

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2000, 05:58:36 ; Search time 17336.7 Seconds

(without alignments)
-3281.814 Million cell updates/sec

Title: US-09-339-352-9

Perfect score: 18738

Sequence: 1 aataaacaatttagttgc.....gagcctcatatcgtgac 18738

Scoring table: IDENTIFY_NTC

Searched: 82193 seqs, -1518192014 residues

Database: GenEmbl.*

Word size: 0

Number of hits that pass the threshold: 1642386

1: gb_dal:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_p11:*
8: gb_p12:*
9: gb_p13:*
10: gb_p14:*
11: gb_p15:*
12: gb_p16:*
13: gb_p17:*
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15: gb_p19:*
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45: gb_p49:*
46: gb_p50:*
47: gb_p51:*
48: gb_p52:*
49: gb_p53:*

50: gb_p13:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18738	100.0	102258	11	HS295C6	297876 Human DNA s
2	1427.4	7.6	184421	42	AC012066	AC012066 Homo sapi
3	1351.4	7.1	223542	40	AC006515	AC006515 Homo sapi
4	1262.4	6.7	126766	11	HSJ154413	AL0495734 Human DNA
5	1244.8	6.6	137111	10	HS20J23	AL022576 Human DNA
6	1242.4	6.6	81746	41	AC011408	AL011408 Homo sapi
7	1235.6	6.6	92171	40	AC004924	AC004924 Homo sapi
8	1222.8	6.5	152077	10	HS13062	AL008627 Human DNA
9	1222.8	6.5	104594	11	HSJ290L14	AL049550 Human DNA
10	1207.4	6.4	134187	40	AC004704	AC004704 Homo sapi
11	1201.2	6.4	94220	41	AC008886	AC008886 Homo sapi
12	1200.6	6.4	165491	11	AC000385	AC000385 Human Chr
13	1199	6.4	35281	11	HS196A2	268165 Human DNA s
14	1183.4	6.3	58645	11	AC002068	AC002068 Homo sapi
15	1175	6.3	171212	41	AC009408	AC009408 Homo sapi
16	1165.8	6.2	179757	40	AC006960	AC006960 Homo sapi
17	1165.6	6.2	140338	43	AC011686	AC011686 Homo sapi
18	1164.4	6.2	150871	32	HSJ1187J4	AL109808 Homo sapi
19	1158.2	6.2	171377	10	CNS01DSX	AL122023 Human chr
20	1154.8	6.2	119427	32	AP000560	AP000560 Homo sapi
21	1146	6.1	155661	11	HS399M14	296074 Human DNA s
22	1145	6.1	98778	32	AC002408	AC002408 Homo sapi
23	1135.4	6.1	176257	40	AC006039	AC006039 Homo sapi
24	1125.8	6.0	182374	44	AC008114	AC008114 Homo sapi
25	1124.2	6.0	297111	42	AC007545	AC007545 Homo sapi
26	1116.2	6.0	93481	40	AF201337	AF201337 Homo sapi
27	1111.6	5.9	169340	40	AC009248	AC009248 Homo sapi
28	1099.4	5.9	215788	40	AC007308	AC007308 Homo sapi
29	1098.6	5.9	154269	41	AC011350	AC011350 Homo sapi
30	1095.2	5.8	41935	11	HSU61B11	273913 Human DNA s
31	1093.8	5.8	211134	40	AC008009	AC008009 Homo sapi
32	1092.6	5.8	133072	10	HS1097P24	AL035258 Human DNA
33	1091.4	5.8	128330	10	HS111D6	AL031056 Human DNA
34	1090.4	5.8	247661	43	AC012154	AC012154 Homo sapi
35	1090.2	5.8	235395	40	AC002470	AC002470 Homo sapi
36	1089.6	5.8	130705	10	HS232L22	273986 Human DNA s
37	1089.6	5.8	39876	11	HSU83C4	270050 Human DNA s
38	1088.6	5.8	105933	33	AC005407	AC005407 Homo sapi
39	1086.6	5.8	108487	11	HS738P15	AL035252 Human DNA
40	1085	5.8	204412	33	HSJ1025A1	AL080312 Homo sapi
41	1083.4	5.8	210680	44	AC013550	AC013550 Homo sapi
42	1081	5.8	177483	11	HSJ148M19	AL050309 Human DNA
43	1078.8	5.8	66817	11	AC005201	AC005201 Homo sapi
44	1072.4	5.7	166182	33	CNS01DUE	AL133241 Homo sapi
45	1072.4	5.7	184659	44	AC016708	AC016708 Homo sapi

ALIGNMENTS

RESULT 1

HS295C6 102258 bp DNA PRI 23-NOV-1999

LOCUS Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains

DEFINITION ESTs, CA repeat, STRs and Cpg island.

ACCESSION 297876

VERSION 297876.1 GI:2562745

KEYWORDS 1q24; Cpg island; repeat polymorphism.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 102258)
AUTHORS Grafham, D.
TITLE Direct Submission
JOURNAL Submitted (27-OCT-1997) Chromosome 1 Project Group
(http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Nov 2, 1997 this sequence version replaced g1:2465042.
COMMENT IMPORTANT: This sequence is the entire insert of clone 295C6.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variations annotated may not be found in the sequence submission
corresponding to the overlapping clone as we submit sequences with
only a small overlap as described above.
This sequence was generated from part of bacterial clone contigs of
human chromosome 1, constructed by the Sanger Centre chromosome 1
mapping group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1/
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The true left end of clone 295C6 is at 1 in this sequence. The true
right end of clone 295C6 is at 102258.
295C6 is from the library RPCII constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/.
FEATURES
source 1.102258
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/map="1q24"
/clone="RP1-295C6"
/clone_1kb="RPC1-1"
891..1180
repeat_region repeat: matches 298..9 of consensus"
/note="Alusq repeat: matches 298..9 of consensus"
1375..1683
repeat_region repeat: matches 303..1 of consensus"
/note="Alusq repeat: matches 303..1 of consensus"
2028..2310
repeat_region repeat: matches 300..1 of consensus"
/note="Alusq repeat: matches 300..1 of consensus"
2612..2903
repeat_region repeat: matches 301..1 of consensus"
/note="Alusx repeat: matches 301..1 of consensus"
complement(4475..4866)
/note="match: 223618 STS containing (CA) repeat"
4625..4670
repeat_region repeat: matches 146..60 of consensus"
/note="23 copies of GT 100 & conserved; differs from
223618"
4766..4897
repeat_region repeat: matches 145..1 of consensus"
/note="MIR2 repeat: matches 145..1 of consensus"
4969..5140
repeat_region repeat: matches 1475..1300 of consensus"
/note="MER42c repeat: matches 1475..1300 of consensus"
5146..5448
repeat_region repeat: matches 302..1 of consensus"
/note="Alufo repeat: matches 302..1 of consensus"
5503..5795
repeat_region repeat: matches 1..299 of consensus"
/note="Alusq repeat: matches 1..299 of consensus"
5797..5925
repeat_region repeat: matches 1265..1124 of consensus"
/note="MER42c repeat: matches 1265..1124 of consensus"
5923..6039
repeat_region repeat: matches 920..804 of consensus"
/note="L1MB6 repeat: matches 920..804 of consensus"
6123..6415
repeat_region repeat: matches 1..292 of consensus"
/note="Alusx repeat: matches 1..292 of consensus"
7799..8099
repeat_region repeat: matches 302..1 of consensus"
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9002..9302
repeat_region repeat: matches 2..303 of consensus"
/note="Alusq repeat: matches 2..303 of consensus"
9692..9983
repeat_region repeat: matches 1..301 of consensus"
/note="Alufo repeat: matches 1..301 of consensus"
10986..11071
repeat_region repeat: matches 146..60 of consensus"
/note="MIR2 repeat: matches 146..60 of consensus"

repeat_region 11583..11766
/note="MIR repeat: matches 262..70 of consensus"
repeat_region 12180..12479
/note="Alusq repeat: matches 1..300 of consensus"
13246..13500
repeat_region repeat: matches 256..1 of consensus"
/note="MIR repeat: matches 256..1 of consensus"
13907..13973
repeat_region repeat: matches 75..141 of consensus"
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13975..14489
repeat_region repeat: matches 526..1 of consensus"
/note="MER1a repeat: matches 526..1 of consensus"
15702..16064
repeat_region repeat: matches 1..371 of consensus"
/note="RHE1c repeat: matches 1..371 of consensus"
16144..16585
repeat_region repeat: matches 9..466 of consensus"
/note="MUTIC repeat: matches 9..466 of consensus"
17173..17534
repeat_region repeat: matches 105..449 of consensus"
/note="LRR2 repeat: matches 105..449 of consensus"
41786..42184
repeat_region repeat: matches 1055..866 of consensus"
/note="L1MA2 repeat: matches 1055..866 of consensus"
AA077391"
repeat_region 18004..18120
/note="3 copies of 39 mer 81 & conserved"
prim_transcript 19377..>21532
/note="match: multiple ESTs; match: N46036 H60052 H12822
T62974 AA283144; match: T57835 F00049 N75628 AA382351
AA300207; match: W37181 N52820 AA337499 W87891 H84729;
similar to endogenous retrovirus POL POLYPROTEIN"
prim_transcript 422156..22928
/note="match: multiple ESTs; match: AA401243 AA258918
AA248892 AA096209 R36280"
repeat_region 23025..23060
/note="3 copies of 12 mer 94 & conserved"
23519..23865
repeat_region repeat: matches 105..449 of consensus"
/note="LRR2 repeat: matches 105..449 of consensus"
24473..24785
repeat_region repeat: matches 1..299 of consensus"
/note="Alusq repeat: matches 1..299 of consensus"
25027..25058
repeat_region repeat: matches 16 copies of 2 mer 88 & conserved"
/note="16 copies of 2 mer 88 & conserved"
25877..25987
repeat_region repeat: matches 788..892 of consensus"
/note="L1PA5 repeat: matches 788..892 of consensus"
26022..26312
repeat_region repeat: matches 1..295 of consensus"
/note="Alusq repeat: matches 1..295 of consensus"
26752..27050
repeat_region repeat: matches 1..299 of consensus"
/note="Alusq repeat: matches 1..299 of consensus"
28012..28312
repeat_region repeat: matches 1..303 of consensus"
/note="Alusq repeat: matches 1..303 of consensus"
28316..29086
repeat_region repeat: matches 109..907 of consensus"
/note="L1ME3A repeat: matches 109..907 of consensus"
29517..29629
repeat_region repeat: matches 262..151 of consensus"
/note="MIR repeat: matches 262..151 of consensus"
29631..29928
repeat_region repeat: matches 1..295 of consensus"
/note="Alusq repeat: matches 1..295 of consensus"
29937..30237
repeat_region repeat: matches 1..301 of consensus"
/note="Alusq repeat: matches 1..301 of consensus"
30238..30315
repeat_region repeat: matches 158..76 of consensus"
/note="MIR repeat: matches 158..76 of consensus"
31096..31287
repeat_region repeat: matches 56..262 of consensus"
/note="MIR repeat: matches 56..262 of consensus"
31289..31379
repeat_region repeat: matches 146..56 of consensus"
/note="MIR2 repeat: matches 146..56 of consensus"
31479..31525
repeat_region repeat: matches 146..95 of consensus"
/note="MIR2 repeat: matches 146..95 of consensus"
33069..33318
repeat_region repeat: matches 262..74 of consensus"
/note="MIR repeat: matches 262..74 of consensus"
35565..35744
repeat_region repeat: matches 1..302 of consensus"
/note="Alusx repeat: matches 1..302 of consensus"
36165..36466
repeat_region repeat: matches 1..302 of consensus"
/note="Alusx repeat: matches 1..302 of consensus"
36992..36944
repeat_region repeat: matches 3..240 of consensus"
/note="MIR repeat: matches 3..240 of consensus"
36999..37299
repeat_region repeat: matches 301..1 of consensus"
/note="Alusx repeat: matches 301..1 of consensus"
37924..38114
repeat_region repeat: matches 1055..866 of consensus"
/note="L1MA2 repeat: matches 1055..866 of consensus"

repeat_region 38108..38475
/note="WTA repeat: matches 425..1 of consensus"
repeat_region 38479..38657
/note="L1M2 repeat: matches 874..687 of consensus"
repeat_region 38658..38957
/note="AlusJ repeat: matches 300..1 of consensus"
repeat_region 38958..39580
/note="L1M3 repeat: matches 699..85 of consensus"
repeat_region 39585..39875
/note="AlusJ repeat: matches 292..1 of consensus"
repeat_region 39877..39951
/note="L1M3 repeat: matches 88..14 of consensus"
repeat_region 39944..40919
/note="L1 repeat: matches 4416..5390 of consensus"
repeat_region 40769..41862
/note="L1P2 repeat: matches 1..893 of consensus"
repeat_region 41764..42556
/note="L1 repeat: matches 5133..4305 of consensus"
repeat_region 42557..42857
/note="Alus repeat: matches 1..301 of consensus"
repeat_region 42876..43925
/note="L1 repeat: matches 4313..3215 of consensus"
repeat_region 44235..44498
/note="MER43 repeat: matches 3..272 of consensus"
repeat_region 44788..44860
/note="MIR repeat: matches 154..82 of consensus"
repeat_region 44933..45220
/note="AlusJ repeat: matches 289..2 of consensus"
unsure 45304..45336
repeat_region 45337..45637
/note="Alus repeat: matches 1..301 of consensus"
repeat_region 45934..46220
/note="Alus repeat: matches 302..14 of consensus"
repeat_region 46817..46935
/note="MIR repeat: matches 35..154 of consensus"
repeat_region 47393..47677
/note="Alus repeat: matches 1..302 of consensus"
repeat_region 48309..48404
/note="MIR repeat: matches 48..140 of consensus"
repeat_region 48620..48862
/note="MER21B repeat: matches 347..102 of consensus"
repeat_region 48865..49159
/note="AlusC repeat: matches 1..296 of consensus"
repeat_region 51182..51467

Query Match 100.0%; Score 18738; DB 11; Length 102258;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 18738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 83581 TACTTCCTTAATTTCTTTTGAGAGAAATTAATCTGTATAATAAATTAATTAATCAATCC 83640

QY 121 ccagagaagtaggcacacatcgtatataatgattccctccctcaagtaagaactctt 180
DB 83641 CCCAGAGAAGTAGGCACACTATGATATATGATTCCTCCCTCCAGTAAGTAAGTAAGTAAGT 83700

QY 181 tggagaagaataggaatttcttactcctcaagcacatatacacacttaacaaactggtat 240
DB 83701 TGGAGACAGAAATAGGAATTTTACTCTCAAGCACATATACACACTTACAAATACTGGATT 83760

QY 241 gagagatcactatatacctctcgtgtaaaaaataaatttcttctgaagtctaaggttca 300
DB 83761 GAGGATTCACCTATATCCCTCTGTGAAAAATTAAGTTCTTACTGAATGCTTAAGAGGTCA 83820

QY 301 taaatacactacattccctactcctccatcccttcatgcaactcccttatggtttg 360
DB 83821 TAAATCTACTACATTTCCCTACTCTTCCCATCCCTTTCATCCCTTTCATCCCTTTATGTTGG 83880

QY 361 ttacttttaaacacccctcttattcccttactacatacaagttacccgtttgcatacat 420
DB 83881 TTACTTTTTTAACACCCCTCTTATTCTTACTTACATACACAAGTTCACTGTTTGCTATCAT 83940

QY 421 gtgacaactagatatacaaatcccttagaatatgttaaaggttaactcttgcacgtatg 480
DB 83941 GTGACAACATAGATACAAATCCTTAGAATATCTTAAGGTTAATCTTTGACATGAGTACG 84000

QY 481 acggccaaaaaaatcattcaattttatttggcgaagctagttctgatttaacactaga 540
DB 84001 ACGGCCAAAAAATCATTTATTTTATTTGTCGCAAGAGTACTGATTTAACATAAGA 84060

QY 541 aactactaagttacatttttagagacataatttaattatcttccacaatgaccttga 600
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DB 84121 AATAGCTATCACTAATAATATAGTACCAAAACATCATGGGTAGATATGTTTTAAAAATGT 84180

QY 661 tgactgaaatacactttggtttgaaatccagagttaaagaacaggttaagaactaaa 720
DB 84181 TGACTGAAATATCACTTTGCTTGAATTCAGAGTAAAGAACAGTAAAGAGACTTAAA 84240

QY 721 tagctaaagatgattgtagagatgataagtttaattactattcttcaagttacaa 780
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DB 84301 GAATAGTACTCTTTTAGATTTTGAAGAAAGCTGTGAATCATCTACTGTAGGACTCATTA 84360

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DB 84421 TAAAAAATACTAGATCCCTTAATCTTAATCTTAACATATATTTATGCTTTCCCAATGAAA 84480

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QY 1021 ttattagctggaagaagctttaaggaagctccaaagctccctcaatttataatgaaga 1080
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Db 85141 GCTCGGCGCTCCCAAGTGGTGGGATTACAGGTGAGCTACCGCGCCAGCTGATATTC 85200
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85501 ATATACCTTATAGAAATATATATGACATATATATCTTAGCTGGCATTAAGATTCF 85560
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QY 2161 atagaacaatatataattgcaactaagttgtaatttaaccatctatgttaacaatctc 2220
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Db	92341	TTCGTCTTTTAAATTAATTAATAGTAGTAACATTAAGAGTACACATAGGTAAGTCTAAC	92400
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Db	92461	TTCGTGTCAATTTGTGTAGTAGTAAGTACGTAGAGTGTGTGATTAATCAATTTAAATGAA	92520
QY	9001	catagctggagctgtgtttttaaacaattacccaataaaagtctgacagtattctcttta	9060
Db	92521	CATAGCTGGAGCTGTGTTTAAACTATTAAACAAAAAGTGTGCGATTTTCTTTTAA	92580
QY	9061	gaattatttgcggaagaagaacttaatttagcttaataaacaagaagttaacatgct	9120
Db	92581	GAATTTATTGGCGGAAGAAGACTTAATTAGCTTATAAACAACAGTTAACTATGTT	92640
QY	9121	ttgcattgatacatattataatttgccttctatctacgttgtagagattgaactgtta	9180
Db	92641	TTGCATGATACATTATTAAATTTGGCTCTTATCTAGTGGAGAGTTTAAGTCTGTGA	92700
QY	9181	tatagctcatattttagtgttcttcttcttcttcttcttcttcttcttcttcttctt	9240
Db	92701	TATAGTCTATATTATTAGTGTCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	92760
QY	9241	agtttaattaaaaataaaccaaacatalacacgtcttctccccccttactccaaactccct	9300
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QY	9361	gaaagccgtgaattacagtttccaaatgtatgtatatacagaaggagttcttactct	9420
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QY	9421	aaataattttagatatgataataataataataataataataataataataataataata	9480
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QY	9481	cctttaaagtggttttcttaagtagtaaaatcttcttgaagtagtcgaacttgaaa	9540
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QY	9541	atgttgcataaagaactaattatgtgccttacccttagtagaaccttaccatgttctc	9600
Db	93061	ATGTTTGAAGAAGCTAATTTATTTGGCTTTACCTTAGTAGACCTTTACAGCTGTATTC	93120
QY	9601	agctctctatactacagtgcttaactcctgtgcttgcattcgaaggaagcaaacatccaca	9660
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QY	9661	ttgttaagtgttgaattagtagtgttcttctttaaataaagtagcttccctccagcttta	9720
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QY	9721	ttgggtataaattgacaattaaaaattgttataattttaaagtgtagaacttgaataactca	9780
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QY	9841	gtggcgaataaagtagcttatacatattataatttataatttataatttataatttata	9900
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QY	9901	cttlttaaagtagtaactcttgcgcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	9960
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QY	9961	ttgggaagcccaaggt	10020
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QY	10021	tggtgaaacccgtgtcttcttcttcttcttcttcttcttcttcttcttcttcttctt	10080
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QY	10081	tgtagctcagctcctctggtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	10140
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QY	10141	gtgcaagtgagccaagatctgtccactgtcaactccaagcttggcgacagaggaactctg	10200
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QY	10201	cgctataataataataataataataataataataataataataataataataataataata	10260

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Qy	10261	aagtcgaattccaaagttagaatcttctcctaagaaatactcctttttaaagaactca	10320
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Qy	10561	taattatctcttctctccctcaagaanaattactctgaanaactctcatatg	10620
Dd	94081	TTAAATATCTCTTCTCTCTCCATCAAGAAATTAATCTCGAAAACTCTCATTAATGT	94140
Qy	10621	tgtgggaatgaagaatgaataattcccgagatgtlaattlaagttlaaagatatgttact	10680
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Dd	94381	CAGGCTGTGGTGCATAGGCAACCTCTATGCTCTACGCACCTCCAGCTCTGTGGCTCAAG	94440
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Dd	94441	GGCACTCTCCCACTCAGCCTCTGTGAATTTTTTTTTTTAAAGATTAATTAACAAG	94500
Qy	10981	tcaagataccgttaggttttaaatglttaaatgtaatagttttccaattactgtatact	11040
Dd	94501	TCAGAGATACCTGTAGGTTTAATAGTTTAAATGTATAGTTTCTCAAAATTAAGTACT	94560
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Dd	94561	AGGTGTAGGTAGTCTTTTGAAATCACTGATTTATTAGCCACACAGATTTTATTATCC	94620
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Qy	11161	ttgctgttttcaatcataatttcttctccttggacaagacactctcaacaatttcaac	11220
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Qy	11221	ctcttaaatlaaagaatagtaattgataaaaaagtaatttlaagttacttccaaggag	11280
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Qy	11281	taattattataagataaanaatggtlaaactatgatttagcagccagtgacaattttt	11340

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Qy	11821	cttaagaagtttaagaagctctcgtgtagcaatgagactatgttacaagtaagctttaggtc	11880
Dp	95341	CTTAGAGGTTTAGAAGCTCTCGTAGCATGAGCTTATGTTACAAAGTATGCTTAGGTC	95400
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OY 16381 tttaaccaatcgaaggttttttttttttttttttttttttttttttttttttttt 16440
Db 99901 TTTACCAATCTAAGGTTTTTTTTTTTTTTTTTTTGAACGAATTTCAATTCGTGTC 99960
OY 16441 cagcgtgagtgcaatggaactcgaactcgaactcgaactcgtcccccgggttcaag 16500
Db 99961 CAGGCTGAGTGATATGACACATCTCAGCTACCTGCAAGCTCTCCGCCGGTTCAAG 100020
OY 16501 tgattctcctgctcgaactcccgagtagctggaattacaggaatggtgccacaacccg 16560
Db 100021 TGATTCCTCTGCTCAGGCTCCGAGTAGTGATTAAGAGCATGTGCCACACACCCG 100080
OY 16561 gctaattttgtgaatttagtagagaacaggtttcaacatgttggccaagctgtgttaa 16620
Db 100081 GCTAATTTTGTAGTTTAAGTAGAGACAGGTTTACCATGTGTGCCAGCTGTCTTAA 100140
OY 16621 ctactgaactcagtgatctgtgccaccccaagctcccaagtgtcgggatacagaagct 16680
Db 100141 CTACTGACCTCAGTGATCTGGCCACCTCAGCTCCCAAAGTGTGGGATTAAGACATG 100200
OY 16681 agctacccgcttgccaactcgaagttttgtggtggaagtttaaggtttctctagata 16740
Db 100201 AGCTACCCGCGCTGCAATATCAAGATTTTGTGGGAGCTTTAGGTTTCTTAAGATA 100260
OY 16741 taagataatcatcagaagaacaggaataattgctcctcctctataatattgaatcc 16800
Db 100261 TAAGATCATATCATGAGAAACAGGATTAATTTGACTCTTCCTTAAATTTTATGACC 100320
|||||

QY	16801	tttggttcattcccttcgcccgatctgtctcgtgttagagacttcaaatctabttgaaag	16860
Db	100321	TTTTGTTTCATTCTCTTGCCGATGGTCTCGTGGTAGGACTTCCAAATGATTAATGAAGAG	100380
QY	16861	tgtggaagtagagcatccctgtcttctctccagttctctcaaggaaatgcttcacatcttc	16920
Db	100381	TGGTGAAGTAGGATCCTCTGTTTCTTCCAGTCTTAAAGGAATGCTTTCATCTTTCC	100440
QY	16921	ctattcagcatbaltgtaagttaacaggtttacacalatalgagcccttaattcttgaagttac	16980
Db	100441	CTATTCAAGTATGAGTTAGTTAGTTACAGGTTTATACATATATGCGCTTATATTGAGGTAT	100500
QY	16981	gactcttcctgccccttagtttaacaaaggtttctctctcaaggaaatgtaattattat	17040
Db	100501	GATCTTCTGTGCTTACTAGTTTACTAAGGGTTTTTCTTATGAAGGAGTGTAAATTTTATTA	100560
QY	17041	aattcctttctcgctcctattaaagatgatcalatgagttcttgccctcattctgttgata	17100
Db	100561	AATTCCTTTTTCCGCTGTATTAAGATGATCATATATGATGTTTGGCCCTTCATTTGTTGATA	100620
QY	17101	tgatgtatcacatcttattgtattgcatatglttgaccatccctgtcatctctgtataaaa	17160
Db	100621	TGAATGATACATTTATTTAGTTTGCAATATGTGACATCTCTTGATCTCTCGATTAATAAA	100680
QY	17161	cccaactgcatcatgltgatataatccctcttgatattggtgttgagattgtgtcttgatatt	17220
Db	100681	CCCACTTGATCATGTGTGTATTAATCTTTTGAATTTGGTGTGAGATTTGGTACAGATT	100740
QY	17221	tctgttagagatctttgcacattgtgtccataaactcgtagttctctcttactctcgtatcc	17280
Db	100741	TTCTGTGAGGATTTTGGATTTGCTTATTAATCTGATAGTTTCTTTTATTTCTGTATCC	100800
QY	17281	ttgtttctgtcctctctcttggtttgtttatcaaggagataatgaccttaaaagtaagt	17340
Db	100801	TTTGTTTTGTCCTTCTTCTTGCGTTTGTATACAGGCGATTAATGCGCTTATAGAAATAGT	100860
QY	17341	taaggagaagccctgctccctgtaatcttttggaaatagttcagaagatctgataactcttc	17400
Db	100861	TAGGAGAAGGCTCTCCTCTGATTTTGGAAATATTTTCAGAGATTTGAAATTAATCTCTT	100920
QY	17401	cttgatcatattgttgaagaatccgctctgaaagccatctgtgtacagggccttctctgttg	17460
Db	100921	CTTGTGATATTGGTATGAATTCGCGCTGTGAAGCCATCTGTGTACTGGCGCTTTCTTGTTG	100980
QY	17461	ggaagatctgataaaatctacgataatctctgctgctcatattatgcttattccagatttc	17520
Db	100981	GGAGATTTGTAATAATTTACTGATTAATCTTGCTGCTCATTAATGGTATTAAGATTTTC	101040
QY	17521	tgttctcttcctggttcaatctctctgtgaagtggtgtttctcgggaagttaacatacttcctg	17580
Db	101041	TGTTTCTTTCGGTTCATCTCTGGTAGGTTGTGTTTTCTGGGAATATCAATTTCTG	101100
QY	17581	taagttcttctcaagttacagagataatgctaatataagtcgtctgtaagatctcttactctc	17640
Db	101101	TAGTCTTTTCAGTTTATAGAGATATATAGTTCATTAATAGTCTGTATGATCTTTGACACTCT	101160
QY	17641	gtggaaatcaagttgtaagtctctctcttctcaatctctgtaattctattcttggtctctctccctc	17700
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QY	17701	tttctctgtgttagctctggaagtggtttatacaaatctttctatctctctgaaggaaacagc	17760
Db	101221	TTTTCTTGCTTAGTCTGGAAGTGTGTTATCAATTTTTTTATCTCTTTAGAGAACACGC	101280
QY	17761	ttttcaattcaatgacctttgttggattcttttttccagttccabatttcaattagttctg	17820
Db	101281	TTTTCATTTTCATTTACCTTTTGTGTGGTTTTTTTTTTCAGTCCAAATTAATTAAGTTCTG	101340
QY	17821	ctcgcgaattatattcttctctctctctgtagattgtgggtttgttttctctctgtttctg	17880
Db	101341	CTTCGATCTTATTTCTTTCTTCTGTAGTTTGGGTTTGGTTTTTCTTCTGTGGTTTTCTG	101400

Oy	17881	gtcctcgagtgctgtccttagatataactgttaactcttctccctttttagtgaaga	17940
Db	101401	gttcctcgagtgctgtccttagatataactgttaactcttctccctttttagtgaaga	101460
Oy	17941	attatctgtctgtctctctcttagcactgcctttgtctatcccaaggttttgatgt	18000
Db	101461	attatctgtctgtctctctcttagcactgcctttgtctatcccaaggttttgatgt	101520
Oy	18001	gtgtttacatcttcaatctgttttcaaaaacatctttttaaattctctgtcctaattctca	18060
Db	101521	gtgtttacatcttcaatctgttttcaaaaacatctttttaaattctctgtcctaattctca	101580
Oy	18061	ttgagcccatgttcattccagagagacatcttctaattgtgtgtatcttgaaggtttga	18120
Db	101581	ttgagcccatgttcattccagagagacatcttctaattgtgtgtatcttgaaggtttga	101640
Oy	18121	aattctcctctgtgatttgatctcagtttctatctcgtctgtctgtctgaagagcattgat	18180
Db	101641	aattctcctctgtgatttgatctcagtttctatctcgtctgtctgtctgaagagcattgat	101700
Oy	18181	gtgattctcagttttaaanaaatctgtctgaagactctgttttctgtgcttaacataagctctg	18240
Db	101701	gtgattctcagttttaaanaaatctgtctgaagactctgttttctgtgcttaacataagctctg	101760
Oy	18241	ctcgagagatctccacatactgtgaatgaataatctgatactctgcagctgtctgataaga	18300
Db	101761	ctcgagagatctccacatactgtgaatgaataatctgatactctgcagctgtctgataaga	101820
Oy	18301	tgttttgtaaatgtcgttaagttcaatcttggtctaaagccagtttaagtcagctgtctc	18360
Db	101821	tgttttgtaaatgtcgttaagttcaatcttggtctaaagccagtttaagtcagctgtctc	101880
Oy	18361	tttgctgactctctgtctcagaatgaatctgtctcgaatgcgtgaagcgtgaagcgtgttgaaatttca	18420
Db	101881	tttgctgactctctgtctcagaatgaatctgtctcgaatgcgtgaagcgtgaagcgtgttgaaatttca	101940
Oy	18421	cactatgtgttgacgtgacatctctctctcttaagcttagtaataactgtttcttaagctct	18480
Db	101941	cactatgtgttgacgtgacatctctctctctcttaagcttagtaataactgtttcttaagctct	102000
Oy	18481	tagtaacctcagctgtcgcgagtgcaaaatagtaattagaattgttatatactctgcgaatt	18540
Db	102001	tagtaacctcagctgtcgcgagtgcaaaatagtaattagaattgtttatattctgtctgaatt	102060
Oy	18541	ggtcctcttaaatatataaagaactctcttagtccttttttttttttttaacgtcttc	18600
Db	102061	ggtcctcttaaatatataaagaactctcttagtccttttttttttttttttaacgtcttc	102120
Oy	18601	tagatgtttttttctcttgcaattttagagatcaactctcaactcttgaacttgaagagatc	18660
Db	102121	tagatgtttttttctcttgcaattttagagatcaactctcaactcttgaacttgaagagatc	102180
Oy	18661	tgaattaaatgttcgaatgtgcgaagaccttttaacatgtaattgtctgaattgtctga	18720
Db	102181	tgaattaaatgttcgaatgtgcgaagaccttttaacatgtaattgtctgaattgtctga	102240
Oy	18721	gacctcacaatctgtgac	18738
Db	102241	gacctcacaatctgtgac	102258

RESULT	2
AC012066	
LOCUS	
DEFINITION	AC012066 184421 bp DNA HTG 29-OCT-1999
ACCESSION	Homo sapiens clone NH0173H09, *** SEQUENCING IN PROGRESS ***, 1
VERSION	unordered pieces.
KEYWORDS	AC012066
SOURCE	AC012066.2 GI:6139271
ORGANISM	HTG: HTGS_PHASE1.
	human.
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
	Eutheria; Primates; Catarrhini; Hominiidae; Homo.

[illegible]

Oy	18344	ttaaagtcacaggtttcttcttgctgagctctcttgcagatgacgtctcaagctgtaagt	18403
Db	43573	ATTAAgTCCAAAGTTCCTTTGCTGATGTGTCTCTCGAANAAGCCTGTCCAACTCGAANAAT	43632
Oy	18404	ggggtgttgaaattccaaactatgty--ttgcagtgatctcttctctttagtctagt	18460
Db	43633	AGGGCTGAGAGCTCTCTGACATTTTGTGGATTAAGAACTCCCTCTCCCTCTTTAGCTTAAC	43692
Oy	18461	aatactgtttatgacctgaactgaactgcagtgctgggtggcaatgatgattgaagatg	18520
Db	43693	AATATTGCTCTAATTAATCTGGGTGCTGTGTGGGGGACAAAT--TATTAAAAATG	43750
Oy	18521	ttataatctctgcgaaattggtctctcttaaatatataaagacgtcttctagtccttt	18580
Db	43751	TTAATCTGTGTGCGAATGACAACTTAATCATATAAAGGAGACCTTTGTGTGTTC	43810
Oy	18581	ttttttttttaaactggtttttagatggttttttctcct	18617
Db	43811	TTATAGTTTGTGCTTGAATCTAATTTTGTCTTAAT	43847

RESULT	3	
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LOCUS	AC006515	223542 bp
DEFINITION	Homo sapiens 3p22-7 PAC RPC15-1053D16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.	PAT 01-APR-1998
ACCESSION	AC006515	
VERSION	AC006515.7	GI:4558536
KEYWORDS	HTG.	
SOURCE	human.	
ORGANISM	human.	
	Homo sapiens	

REFERENCE	1 (pages 1 to 223542)
AUTHORS	Muzny, D., Arenson, A.D., Bouck, J., Bunac, C., Chen, J., Chen, Z., Colpepper, P., Ding, Y., Dugan, S.P., Durbin, K.J., Forcum, J., Ganes, R.P., Garcia, C., Garcia, D.K., Gorrell, H., Gorrell, L.L., He, X., Hernandez, J., Jackson, L.E., Kondajewski, N., Leal, B., Licharge, O., Liu, W., Logan, O., Lu, J., Martinez, C., Moore, S., Moorish, T., Nguyen, N., Oswal, G., Pampell, L.R., Parish, B.J., Perez, L.M., Rashid, N.D., Rives, C.M., Scherer, S.E., Shen, H., Simon, M.L., Vo, O.K., Wei, Y., Williamson, A.L., Worley, K., Zhou, X., Naylor, S.L. and Gibbs, R.A.
TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (pages 1 to 223542)
AUTHORS	Morley, K.C.
TITLE	Direct Submission
JOURNAL	Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	3 (pages 1 to 223542)
AUTHORS	Morley, K.C.
TITLE	Direct Submission
JOURNAL	Submitted (01-APR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT	On Apr 2, 1999 this sequence version replaced g14454420. INFORMATION: http://www.hgsc.bcm.tmc.edu/or_email/gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,

unpublished.) for Human and Mouse sequences. Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensu splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: this sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

FEATURES	Location/Qualifiers
source	1. .223542

Repeat_Region	/organelle="Homo sapiens /db_xref="taxon:9606" /clone="RRC15-1053D16" /chromosome="3p22-7" complement(65, .686) /rpt_family="MLRG" complement(872, .1070) /rpt_family="MLRG" 1076, .1373
Repeat_Region	/rpt_family="AluJb" complement(1378, .1441) /rpt_family="MLRG" complement(2134, .2163) /rpt_family="TAA)n" 2512, .2600
Repeat_Region	/rpt_family="MIR" 3310, .3611 /rpt_family="AluSq" 3877, .3916 /rpt_family="L2" 4184, .4451
Repeat_Region	/rpt_family="LINE3" 4434, .4801 /rpt_family="MER7A" 4836, .4942
Repeat_Region	/rpt_family="LINE3" 5055, .5174 /rpt_family="FLAM_C" 5189, .5485
Repeat_Region	/rpt_family="AluJb" 5486, .5947 /rpt_family="LINE3" complement(6589, .6682)
Repeat_Region	/rpt_family="AluJb" 7392, .7481 /rpt_family="(TA)n" complement(7495, .7795)
Repeat_Region	/rpt_family="AluY" complement(7807, .8100) /rpt_family="AluXs" complement(8643, .9142)
Repeat_Region	/rpt_family="AluXs" 9835, .10116 /rpt_family="AluXs" complement(10937, .11242)
Repeat_Region	/rpt_family="AluSq" 11347, .11628 /rpt_family="L1R16C" 11347, .11628

	repeat_region	33897..33973	/xprt_family="TL2"	
	repeat_region	34887..35018	/xprt_family="Mir"	
	repeat_region		complement(35269..35369)	
Query Match		7.1%: Score 1331.4; DB 40; Length 223542;		
Best Local Similarity	63.5%;	Pred. No. 1.5e-209;		
Matches 3078; Conservative	0; Mismatches 1151; Indels 616; Gaps 4			
QY	14280	tttcattcatttttttttggatgagatctcaactctgtccgcacgaagtcgtagtgcagtg	14339	
Db	176406	TCTTTTTTTTTTTTTTTTTGAGATGAGAGTCACATCTGTGGCCAGGCTGAGATGCAGTG	176465	
QY	14340	gtgagatctcggtctactgcagaattccgcctcogaagtltaacgccattctctgcctcag	14399	
Db	176466	GTCGGATCTCGGCTCACGTCAGACTGCCGCCGCCCGGGGTCA-GCCATTCTCCTCCCTCAG	176522	
QY	14400	cctcccaagtagttgggaatacaagtgccccgcacacacctgaacttttttttgt	14459	
Db	176525	CCTCCTGAGTAGCGGGGACATACAGGCCACCACACCATGCCCCGCTAA---TTTITGT	176580	
QY	14460	atttccaagaagaacaagggtttcacagtgtagaccagaatgagccctgatccccagacct	14519	
Db	176581	ATTTTATAGTAAGAAGCGGGGTTTCCACCGTGTAGCCAGAGATGTTTCATCTCCGACCTC	176644	
QY	14520	gtgactctgcggccctcgagccctcccacaaagtctggagatcacaggggtgagccacacgcc	14579	
Db	176641	ATGATGACCCCGGCTCGGCCCTCCCAAAGTGCTGGATGACAGCGGTGAGCACACCTTGCC	176700	
QY	14580	agcctgatt-----	14589	
Db	176701	TGGCCCATGTGATCATTCCTATGCCCTTGTGCTCTTAGCTTAGCTCCACATATCAGT	176760	
QY	14589	-----	14589	
Db	176761	CAGAACATAGCATGCTGTTGTTTCCATTCCGTAGCTTCTTCACTTACAATAATATGTTCC	176822	
QY	14589	-----	14589	
Db	176821	AGTCTCATCTGAGTTGTGTCGAATAAGCCATTAACTTATCTCTTTTATAGCTGAGACATAT	176880	
QY	14616	tcaatttgtagtatgagctgaatgatat	14615	
Db	176881	TTTCATCATATGTAATATATAC-A-TTCTTTATTCACGCTGGTGAATGAGGCACTCTGGT	176933	
QY	14676	tgaattcatatctctgtctgtgtgaafagtcgcagtaaacaatcgcgtgcacatact	14735	
Db	176939	TGGTTCACAGATTTTGCAGATTGTGAATTTGTGCTGCTTAACACAGCATGTGCAAGTATCT	176999	
QY	14736	tttagataataattctcttt-cttttglaaaaalctagtagtggagattgctaagtg	14794	
Db	176999	TTTTCATATAATGACTTCTTCTTCTCGGTAGATACCCAGTAGTGGAATGCGTAGTCA	177058	
QY	14795	aagaatagttctattttaattctcttgagaaatctccatactgtttccctagaagtgct	14854	
Db	177059	AATGTGATGTTCTACTTTTATGTTCTTTAAGAGATCTCCACACTGTTTCCATATAGGCTGT	177118	
QY	14855	actaatctaacctcccaacaatglatataaggtctcccttttccataatgaataacaa	14914	
Db	177119	ACTGATTACTTCTCCACACAGACTGTGGAAGTGTTCCTCGATCAGTCACACACAA	177178	
QY	14915	ca-----ttgtctgtcttttaataaagaacattctgcacgaagataagtgatctc	14967	
Db	177179	CATCTACTAGTTTATTTGACTTTTGCATTATATGAGCCATCTCTCGACAGATAAGTGGTATCAC	177238	
QY	14968	atttgtgaatttgattgcattctctctataagacggtgaatgttgagcaatltttcataat--	15026	
Db	177239	ATTGTGATTTTGAATTAATTTTCTCATATCATTAAGTATGTTGAGCATTTTTCATATGT	177298	
QY	15026	-----acctgtgggtgtatgacttttgaaaaabtgatcatcatcagtggttggccactttt	15080	
Db	177289	TCAATGCCATTGTATATCTCTCTTTTGAAGAAATGTCTATATCATGCT-CCTTATCCACCTTTT	177355	

Dh	179486	CGAGGAGGATGCTTTCAACTTTTCCCATTCAGATATATTTGGCTGTGGTTGTGCATA	179545
Oy	16986	tatggccttatatttgg-----agatatgactcttctgtgcctagtattactaagg	17008
Dh	179546	GATGGCTTTATTTTCATTGTATGTAAATAGCATATCCCTGTATACCGATTTCCTAGAG	179605
Oy	17009	ttttcttatgaaggaatgttgaatttatataattcttcttcgcgttcattaaatga	17068
Dh	179606	TTTAAATCATTAAGGAGATGCTGGATTGGTTGGTAATGCTTTTTCGATCTATTCAGATAA	179665
Oy	17069	tcaatagtcttttgccttcacatctcgttgaatgatgatcattatgatattgacata	17128
Dh	179666	TCATGTGATTTTGTTTTAAATTCGTATTATGTATATGCTATGATATTTATGACTTCATA	179725
Oy	17129	tgttgacctatcccttgcatccctcgttatataaaacctgatcataggtgatattcttt	17188
Dh	179726	TGTAAACCATTTCTGCATCCCTGTGTGAATACCATTTATCATGTGTATATCTTTT	179785
Oy	17189	tgaattggttgattatggtttgctagtatttggctgaagattttgcatctgtctca	17248
Dh	179786	TGATATGTGTATTAATTGATTTCATTCCTAGTATTTGGAAAGATTTCGTATGTCTCA	179845
Oy	17249	ttaactgtagttctcttttatcgtatcccttggtttgttgccttccttggtttgt	17308
Dh	179846	TCA-----GGGATATCAACAGTATGTTTCTTTTGGTATGC-1798884	
Oy	17309	tatacgggcgataatgacctatagaataagttagaagag---gcctgccttgattt	17365
Dh	179884	-----GGGTGTGTGCTGCCTTAATATGAATATGAAATGAGGAGGGTCCCTTTTCTTTTCTT	179938
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Dh	179939	GTCGAATGTGTCAAAAGGATGCTGCCAATCTCTTTTAAATGTCGTGAGAAATTCGC	179998
Oy	17426	tgtgaagccatcgtgacatcgggcttctctctgtgtggagatgtglaaanaattacgataa	17485
Dh	179999	TGTGAATCATCTGCTGCTCGACTTATTTTGTGAAATAATTT--AAATACCATTTCA	180056
Oy	17486	ttctctgctcccatattgtgtctcttaagatttcttctctctcgttcattcttght	17545
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Oy	17546	aggtgtgttttctcgggaatgatcatctccgtcgaagtttctagtttaagatat	17605
Dh	180117	GGGCTGATGTTTCAGAGAAATTAATCATCTCTTCAGTTTCAGTTTATGTGTGCA	180176
Oy	17606	a---gtccatatagtctgtagatcatc-ttgtactctctgtgaatcaagtgtacgtc	17661
Dh	180177	AGGCTTCATATAGTAGCCTTGAAATATCTACTGTAATTCATTGGTGTCAGTGAATATCT	180236
Oy	17662	ccatttcaatt---ctgattatattggcctctccctcctctcttctgtttagtcg	17717
Dh	180237	CCCATTCATTTTAAATGAGAGTATTTGGATTTCTCTCTCTTTCTGGTTATCTT	180296
Oy	17718	gaaagtggttatacaattttttatctctcttgaggaaaccaagctttcattcaattgacc	17777
Dh	180297	GCTATGTGCTATCAATTTATTTATTCCTTTTCAAAATATACGCTTTTAAATTTATATTC	180356
Oy	17778	tttggtaggttttttttttgaagccaatcttaatttggtctgctcgaact---ttatt	17834
Dh	180357	TTTTGTATTTTGTGTTCA-----AATTCATTATGTTTCGCCGATCTGGTTATT	180410
Oy	17835	tctttctctgcagcttttgggttggtttcttctcgtgttctcgttccctcgaagtcg	17894
Dh	180411	TCCTTTCTCTGCTAGGTTTAGTTTGTTGTTCTTGTTCCTCTCTAGTTCCTTGGGGTGT	180470
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Dh	180471	GTCCTTAGAATGTCAGTTTGGTTCCTTCAAGCCTTTTGAATGATAGCTTTAGGGCTATG	180530
Oy	17954	-----tctctcttagcactgcttctgtcgtatcccaaggttttggatgttgttcttaaa	18009

Dh	180531	AACTTCCTCTTACACAGGCGCTTGGTGTAATCCAGAGGTTTGATAGGTGGTCATTA	180590
Oy	18010	tttccatttgttcaaaaaacatttttttaaatttcytccttaatttccttaattgcacc	18069
Dh	180591	TTGTGTTCACTTGGCAGA--ATTTTATTAATTCATCTGTGAATTCGGTTTGACCAC	180647
Oy	18070	ttgtcattccagagcagctggttttaattgctgtatgttgatttgaaagttgaaattctc	18129
Dh	180648	TGCTCATTCCAGACAGGTTATTTCTTTCCANGTGTTTCACAGGTCGTAAACATTCCT	180707
Oy	18130	ttggtaattgacttcttaatttatctcgtctgtctcgaagaagcacttgatgattca	18189
Dh	180708	TAGGAGGTGATTTCCAGGTTGTGTCCTGGGTC--GAAGGCTGTGATTAATTCA	180765
Oy	18130	gttttaaaaaattgttgagaacttgtttgtgtgcttaacatatgctccttgagaa	18249
Dh	180766	ATTTTGTAACTTATTATGA-AGCCGCTTTTGTCGCATATATGGCTATCTGGAAGA	180824
Oy	18250	tgttccatattcgtatgaaaaatgttatatcttcgcagctgttcggatagaacttgta	18309
Dh	180825	ATTCCACGTCTCCTTGTAATGAATGTGTATTCTGAAAGTTGTGGATGAATGTTCTGA	180884
Oy	18310	aagtcctgtaagttcatcttgcttaagaagctcagtttaagtcagtgcttcttgcat	18369
Dh	180885	TATATCTGTATTAATTCATTGTTTCCAGGATATCTTAATATCATGTTTCTATGTTGAC	180944
Oy	18370	tcttcttgcttaagatctgcttctaattgctgaatggtggttgtaatttcacac---tat	18426
Dh	180945	TTTCTGCTTTATATACCTGTCTTACTGCTGTGCAGGGAGTCAAGTCCCCCACTATAT	181004
Oy	18427	tgcttgccagtgatacctcttctcttagtcctagtaaacctgttttaagccttagtac	18486
Dh	181005	TGTGTGCTGTCTATGTTCATTTCTTAGCTCTATTAGTAATTTGTTTATAATTGGAGC	181064
Oy	18487	tccagtgccgggtgcaaatatgtaatttagaattgtatactatctctgctaattggtc	18546
Dh	181065	TCCAGTGTAGTGCCAAATATG--TTTAAATGTGTGATTTTCCGTGTGATGTGGCT	181122
Oy	18547	tttaatatataaagaacttctcttagtcccttttttttttttttttttttttttttttt	18551
Dh	181123	TTTACCATTAATAATGTCCTTTTGTCTTTTAACATANTGT	181167

RESULT	4				
LOCUS	HSJ154J13	/c			
DEFINITION	Human DNA sequence from clone 154J13 on chromosome Xq26.1-26.3, complete sequence.				
ACCESSION	AL049734				
VERSION	AL049734.11				
KEYWORDS	GT:5791525				
ORGANISM	human.				
SOURCE	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 126766)				
TITLE	Bird.C.				
JOURNAL	Direct Submission				
COMMENT	Submitted (28-Aug-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunquerey@sanger.ac.uk Clone requests: clonequest@sanger.ac.uk On Aug 27, 1999 this sequence version replaced gi:5777846. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: EMBL, EMBL; SW, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence is				

the entire insert of clone 154J13. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/ChrX>

154J13 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/VECTOR:pcypac2>.

FEATURES

source

1.126766

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="X"

/map="q26.1-26.3"

/clone_lib="RPCI-1"

/clone="RP1-154J13"

BASE COUNT 41677 a 24251 c 24278 g 36560 t

ORIGIN

Query Match

6.7%; Score 1262.4; DB 11; Length 126766;

Best Local Similarity 62.4%; Pred. No. 3.3e-198;

Matches 2613; Conservative 0; Mismatches 1361; Indels 214; Gaps 32;

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QY 14582 cctgattcattcttctgtatgctgtaagtagtattccattggtatatacacacattt 14641
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Db 64506 CAGGAATCTCATATTTTATGCTGATGATTCATGATGATGATGATGATGATGATG 64447

QY 14642 cttaccgttcaacccttgatgagacacttaggttgatccattcttgctgttgaa 14701
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Db 64446 CTTAATCCAGTCATCATGTGTGGAGCTGTGGCTGTGGCTGTGGCTGTGGCTGTG 64387

QY 14702 tagtgcgcagtaaacactgctgacacatactt-tagaataatattcttcttct 14760
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Db 64386 TAGGCCACATAAACAATACGTGTCATGTCTTTATAGAGATGATTTATAGTCTT 64327

QY 14761 ttgttaaaacactagtggtgagatgctagatggaagatagttctatctttaa 14820
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QY 14821 gagaacatcctacactgtttccatagagctgacataattatccacacacatgta 14880
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QY 14881 tataaggttcccttttttttccacatgaacaacacacacacacacacacacac 14933
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Db 64206 TAAAGTGTTCCTGTTCTCCACATCCTCTCCACACCTCTGTTTCTGATCTTTAT 64147

QY 14934 aaaaagcattctgactagatgaagtgatatactcatctgtaattgatttgacttct 14993
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QY 14994 taagactggtgaagtgtgacatttttccataaccctgttg- - - - -gtgtgcttc 15045
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QY 15046 tgaaaaatgctatctcgtgtgttttgctacttttaataagatggttagattttttg 15105
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Db 63968 TTGTAAATTTGTTGATGTTCTTTAGATTTCTGATTTAGATTTAGATTTAGATTT 63909

QY 15166 tttagcagatatcttctgctacacagagattggtgtctcttcaactgttattctt 15225
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QY 15272 - - - - - 15272
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Db 63788 CATGTCTTTTGTTGTTTATAGATGATGATGATGATGATGATGATGATGATGATG 63729

QY 15272 - - - - - 15272
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Db 63728 GCCTAGGTTTCTTCTAGGGTGTATGTTTATGTTTATGTTTATGTTTATGTTTAT 63669

QY 15320 ccttgattgattttatgattagtagagagaagaagattcaattgacattctgtcata 15379
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Db 63668 TCTTGAATTTATTTTCTATTAAG-GTCTAAGAAAGGATGATGATGATGATGATGATG 63610

QY 15380 tggatatctaatttctcagacacattgattgaagagggttccgttccacagtgatgt 15439
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Db 63549 TTTTCTAGGTTTGTCAAGATGATGATGATGATGATGATGATGATGATGATGATG 63490

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QY 15800 gggatgttttccatttg- - - - -tgtaagtataattctttagcgtgtgttgtagttc 15855
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Db 63190 GGAATGTTCTTCATTTGTTTCTATCTCTTTTATTTTATGAGACAGTGTGTTG 63131

QY 15856 tcccttg- - - - -taggaatttaccctctgtttaaatatattcctaagttgtgtgt 15910
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QY 15911 atgtgtgttttaataatttcttcttcttcttcttcttcttcttcttcttcttcttct 15968
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Db 63070 GATTATCTCAATGATGACAAAGAGGCTTTGACAAATTAACCAACCTTCTAGTAA 63011

QY 15968 - - - - -ctgtaccacagcgtgagatgacagtgacacatctcoggttcttaacctccgctcc 16025
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QY 16191 ctggtcctcccaagtgctgattcaaggcgtgagcaccacaccccggtctttttt 16250
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Qy	18360	ctctcgtatctcttctgtcagaagtcgtccgtcaacgctgaagtgaggtgtgtaatttc	18419
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Qy	18420	aacacta---tttgtgtgcagtgatcatctctctcttaggtctagtaactgtttatga	18476
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Qy	18477	ctcttaagtaactccagtggtcgcgggtgcaaatatgtat---ttagaattgttatattctt	18532
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Qy	18533	gttgattggtctctcttataataataaagcctttctaagccttt	18580
Db	60391	gtttgacacagccctttttatcactaatatattgtccctctttgtcttttt	60344
RESULT	5		
LOCUS	HS20J23		
DEFINITION	HS20J23	137111 bp	DNA
			PRI
			23-NOV-1999
			Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2
			Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1)
			(ras-like protein TC25) EST, CA repeat, STS, CPG island, complete
			sequence.
ACCESSION	AL022576.1	GI:3288426	
VERSION	AL022576		
KEYWORDS	HTG; P21-RAC1; ras-like protein TC25; repeat polymorphism.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
	Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 137111)		
AUTHORS	Pearce,A.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-JUL-1998) E-mail enquiries: humquerry@sanger.ac.uk		
COMMENT	Clone requests: clonequests@sanger.ac.uk		
	On Jul 4, 1998 this sequence version replaced gi:3250824.		
	During sequence assembly data is compared from overlapping clones.		
	Where differences are found these are annotated as variations		
	together with a note of the overlapping clone name. Note that the		
	variation annotation may not be found in the sequence submission		
	corresponding to the overlapping clone, as we submit sequences with		
	only a small overlap as described above. This sequence is the		
	entire insert of clone 20J23. This sequence has been finished		
	according to sequence map criteria as follows. An attempt is made		
	to resolve all sequencing problems, such as compressions and		
	repeats, but not necessarily within known annotated human repeat		
	sequence elements (e.g. Alu). Where the sequence is ambiguous,		
	there is an annotation using the 'unsure' feature key.		
	This sequence was generated from part of bacterial clone contigs of		
	human chromosome X, constructed by the Sanger Centre Chromosome X		
	Mapping Group. Further information can be found at		
	http://www.sanger.ac.uk/HGP/ChrX		
	20J23 is from the library RPc11 constructed at the Roswell Park		
	Cancer Institute by the group of Piter de Jong. For further		
	details see http://bacpac.med.buffalo.edu/VECTOR.pcrPAC2.		
FEATURES	Location/Qualifiers		
Source	1..137111		
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	/map="q26.2-27.2"		
	/clone="Rpi-20J23"		
	/clone_lib="RPC1-1"		
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	complement(442..743)		
	/note="AluX repeat; matches 302..1 of consensus"		
	complement(746..1024)		
	/note="V1MK1 repeat; matches 488..206 of consensus"		
	999..1371		
	/note="WSTD repeat; matches 1..394 of consensus"		

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repeat_region	complement(2466..2568)	
repeat_region	/note="ERR38 repeat: matches 109..4 of consensus"	
repeat_region	complement(3029..3355)	
repeat_region	/note="L1M62 repeat: matches 910..581 of consensus"	
repeat_region	3382..3687	
repeat_region	/note="ALUv8 repeat: matches 1..303 of consensus"	
repeat_region	3688..3713	
repeat_region	/note="13 copies 2 mer ga 92% conserved"	
repeat_region	4610..4869	
repeat_region	/note="MIR repeat: matches 3..261 of consensus"	
repeat_region	6094..6242	
repeat_region	/note="MIR repeat: matches 2..151 of consensus"	
repeat_region	6244..6551	
repeat_region	/note="ALUv8 repeat: matches 1..308 of consensus"	
repeat_region	7075..7340	
repeat_region	/note="ALUv8 repeat: matches 1..269 of consensus"	
repeat_region	7348..7562	
repeat_region	/note="MIR repeat: matches 33..245 of consensus"	
repeat_region	7563..7898	
repeat_region	/note="1HXB repeat: matches 28..364 of consensus"	
repeat_region	complement(7985..8367)	
repeat_region	/note="MLTIB repeat: matches 390..1 of consensus"	
repeat_region	complement(9128..9394)	
repeat_region	/note="ALUv8 repeat: matches 292..2 of consensus"	
repeat_region	complement(9943..10412)	
repeat_region	/note="L1M66 repeat: matches 1047..559 of consensus"	
repeat_region	complement(10434..11316)	
repeat_region	/note="L1P62 repeat: matches 891..1 of consensus"	
repeat_region	complement(11167..11451)	
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repeat_region	11493..11538	
repeat_region	/note="73 copies 2 mer ta 89% conserved"	
repeat_region	complement(11569..12007)	
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repeat_region	complement(12010..12308)	
repeat_region	/note="ALUv8 repeat: matches 302..1 of consensus"	
repeat_region	complement(12309..12352)	
repeat_region	/note="L1M88 repeat: matches 113..70 of consensus"	
repeat_region	complement(12353..12436)	
repeat_region	/note="ALUv8 repeat: matches 291..208 of consensus"	
repeat_region	complement(12438..13219)	
repeat_region	/note="L1 repeat: matches 5316..4522 of consensus"	
repeat_region	13425..13456	
repeat_region	/note="16 copies 2 mer tt 84% conserved"	
repeat_region	complement(13460..13735)	
repeat_region	/note="ALUv8 repeat: matches 301..14 of consensus"	
repeat_region	complement(14013..14115)	
repeat_region	/note="MIR repeat: matches 216..122 of consensus"	
repeat_region	14133..14172	
repeat_region	/note="70 copies 2 mer ac 98% conserved"	
repeat_region	14304..14366	
repeat_region	/note="MIR2 repeat: matches 84..146 of consensus"	
repeat_region	complement(16096..16450)	
repeat_region	/note="L1M83 repeat: matches 676..321 of consensus"	
repeat_region	complement(16961..17023)	
repeat_region	/note="MIR2 repeat: matches 146..84 of consensus"	
repeat_region	18418..18691	
repeat_region	/note="ALUv8 repeat: matches 1..289 of consensus"	
repeat_region	complement(22513..22719)	
repeat_region	/note="MIR repeat: matches 218..4 of consensus"	
repeat_region	complement(23273..23570)	
repeat_region	/note="ALUv8 repeat: matches 300..3 of consensus"	
repeat_region	complement(24114..24784)	
repeat_region	/note="MIR2 repeat: matches 146..76 of consensus"	
repeat_region	25015..25073	
repeat_region	/note="MIR2 repeat: matches 40..97 of consensus"	
repeat_region	25807..25941	
repeat_region	/note="MIR2 repeat: matches 24..146 of consensus"	
repeat_region	25992..26090	
repeat_region	/note="MIR repeat: matches 91..188 of consensus"	
repeat_region	complement(26496..26636)	

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complement(2464. .2568)
/note="ERRA repeat: matches 109. .4 of consensus"
complement(3029. .3355)
/note="L1ME2 repeat: matches 910. .581 of consensus"
3382. .3687
/note="L1usg repeat: matches 1. .303 of consensus"
3688. 3713
/note="13 copies 2 mer ga 92% conserved"
4610. .4869
/note="MIR repeat: matches 3. .261 of consensus"
6094. .6242
/note="MIR repeat: matches 2. .151 of consensus"
6244. 6551
/note="AluBb repeat: matches 1. .308 of consensus"
7075. .7340
/note="Alusg repeat: matches 1. .269 of consensus"
7348. .7562
/note="MIR repeat: matches 33. .245 of consensus"
7563. 7898
/note="THE1B repeat: matches 28. .364 of consensus"
complement(7965. .8367)
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11493. .11538
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complement(12010. .12308)
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complement(12309. .12352)
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complement(12438. .13219)
/note="L1 repeat: matches 5316. .4522 of consensus"
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complement(13460. .13735)
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complement(14013. .14115)
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18418. .18691
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complement(24714. .24784)
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25015. .25073
/note="MIR2 repeat: matches 40. .97 of consensus"
25807. .25941
/note="MIR repeat: matches 24. .146 of consensus"
25992. .26090
/note="MIR repeat: matches 91. .188 of consensus"
complement(26496. .26636)

repeat_region	/note="MIR repeat: matches 206. .58 of consensus" 27159. .27176 /note="19 copies 2 mer gt 100% conserved" 28069. .28101 /note="MIR2 repeat: matches 114. .146 of consensus" 28699. .28895 /note="MIR repeat: matches 1. .202 of consensus" 28896. .29430 /note="MIR2D repeat: matches 1. .534 of consensus" 29439. .29487 /note="MIR2CA repeat: matches 455. .503 of consensus" 29489. .29557 /note="MIR2 Internal repeat: matches 2. .70 of consensus" 29556. .29827 /note="MIR2 Internal repeat: matches 272. .535 of consensus" 29825. .30065 /note="L1 repeat: matches 5150. .5389 of consensus" 29917. .30434 /note="L1P2C repeat: matches 1. .517 of consensus" 30437. .30735 /note="A1Y repeat: matches 1. .299 of consensus" 30736. .31114 /note="L1P2S repeat: matches 510. .888 of consensus" 31125. .31200 /note="MIR2 Internal repeat: matches 537. .609 of consensus" 31217. .31283 /note="MIR2G repeat: matches 321. .388 of consensus" 31231. .31283 /note="MIR2C8 repeat: matches 453. .501 of consensus" 31561. .32214 /note="MER42C repeat: matches 573. .1254 of consensus" 32196. .32310 /note="MER42C repeat: matches 1292. .1404 of consensus" 32309. .32350 /note="MER42C repeat: matches 1489. .1530 of consensus" /note="MER42C repeat: matches 1489. .1530 of consensus" 32614 /note="MIR repeat: matches 153. .110 of consensus" 32808. .32875 /note="L1P4T repeat: matches 829. .892 of consensus" 33035. .33138 /note="MIR2 repeat: matches 43. .146 of consensus" 33421. .33615 /note="MIR repeat: matches 12. .206 of consensus" /note="MIR repeat: matches 12. .206 of consensus" 34003 /note="A1USX repeat: matches 297. .1 of consensus" /note="MIR repeat: matches 301. .1 of consensus" 35069. .35315 /note="MIR repeat: matches 1. .257 of consensus" /note="MIR repeat: matches 1. .257 of consensus" 37050. .37655 /note="MIRIE repeat: matches 568. .1 of consensus" /note="MIRIE repeat: matches 568. .1 of consensus" 37846. .38151 /note="A1UO repeat: matches 302. .1 of consensus" /note="A1UO repeat: matches 302. .1 of consensus" 38623 /note="A1UO repeat: matches 294. .1 of consensus" 39065. .39370 /note="A1UO repeat: matches 1. .269 of consensus" /note="A1UO repeat: matches 1. .269 of consensus" 39821. .40052 /note="A1USX repeat: matches 292. .38 of consensus" /note="A1USX repeat: matches 292. .38 of consensus" 40265. .40449 /note="A1USX repeat: matches 302. .122 of consensus" 40451. .40549 /note="A1USX repeat: matches 4. .102 of consensus" 40951. .41602 /note="L1M5 repeat: matches 267. .921 of consensus" /note="L1M5 repeat: matches 267. .921 of consensus" 41614. .41878 /note="A1USG repeat: matches 300. .38 of consensus" 42197. .42488 /note="A1U3b repeat: matches 1. .291 of consensus" 43197. .43411 /note="MER20 repeat: matches 2. .218 of consensus"
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QY	14642	ctttaccgttatccatttgtttggscacttagtgtagtaccatatcttggttgtgaa	14701
DB	59785	CTTTAATTAGTGATGGATTGTGATGGGCATTGGGGTGGCTCCAAAGCTTTGGTATTGTGA	59844
QY	14702	tagtgcctcagtaaacacacactggtgacacatacctttaagacatactaattctt-	14760
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DB	59905	TGGGATATATACCCCATATGAGATGGATGGCGGTCAAAATGTAATTCCTGCTCTACATCCTT	59964
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DB	60085	GATTCGCATTCTAACTGGTGTAAGATGCTATCTCATTTGGTTTTGATTTCATTTCCT	60144
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DB	60145	AATGACCACTGATGATGATGAGCTCTTTTATATGTTGTGGCCACATAAATGCTCTCTT	60204
QY	15046	tgaaaaatgctatcacatgtylcttgcctactctttaaagaattgttagaattctt	15105
DB	60205	TGAGAAGATATCTGTTATATATCATTTACCCACATTTTGTAGGGGTGTTGG--TTTTTTC	60262
QY	15106	tgtgtgaatcggttgaagtlccttggtagtcttgatgatatagtcocctggttgaga	15165
DB	60263	TGTGAATTTGTTAAGTTCCTGTGAGATCTGTGATATTAATTCCTTGTGCATGAGATAC	60322
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DB	60323	ATTGCAAAAATTTTCTCCCATTTCTTTAGG-TTGCCCATTCACCTTACAGATAGCATCTT	60381
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DB	60621	GGCTAGCCAGTTTTCCTCCACACCAATTTATGAAATAGGGCACCTTTCCTCCATTCCTG	60680
QY	15441	cttgtagcgttttgtaaacacagttgctcgaagttagtggccttctttcttggtctc	15500
DB	60681	TGTGTACAGTTTGTCAAAGATCAGATGGTGTATAGATATGTGTATTTCTGTAGGCTTC	60740

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QY	16760	aacagagaaatttgaactctctctcttataattgaatgaccttctgtttcattctctgc	16819
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ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS	Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE	1 (bases 1 to 81746)
JOURNAL	DOE Joint Genome Institute.
REFERENCE	Sequencing of Human Chromosome 5
AUTHORS	Unpublished
TITLE	2 (bases 1 to 81746)
JOURNAL	DOE Joint Genome Institute.
REFERENCE	Direct Submission
AUTHORS	Submitted (06-0CC-1999) Production Sequencing Facility, DOE Joint
TITLE	Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
JOURNAL	www.jgi.doe.gov.
COMMENT	* NOTE: This is a 'working draft' sequence. It currently * consists of 10 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
	* 1 744: contig of 744 bp in length
	* 745 791: contig of 47 bp in length
	* 792 2306: contig of 1515 bp in length
	* 2307 4822: contig of 2516 bp in length
	* 4823 7872: contig of 3050 bp in length
	* 7873 11199: contig of 3327 bp in length
	* 11200 14451: contig of 3252 bp in length
	* 14452 23678: contig of 9227 bp in length
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Db 19979	TTATCCACTCATCTGATGATGATGCGCATTTGACACCGCTTCCATTTTTCGCGCTGCAAT 19920
QY 14704	gtgcgcgcgtaaacactactgtgacacatactcttttagtatataattcattctctttt 14763
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QY 14764	gtaaaactcagtagtgaggatcgcacagatgaaaagatagttcattcattcattcctgag 14823
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homindae; Homo.
 REFERENCE 1 (bases 1 to 92171)
 AUTHORS Sulston,J.E. and Waterston,R.
 TITLE Toward a complete human genome sequence
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
 MEDLINE 99063792
 REFERENCE 2 (bases 1 to 92171)
 AUTHORS Edwards,J.
 TITLE The sequence of Homo sapiens PAC clone DJ0903602
 JOURNAL Unpublished (1999)
 REFERENCE 3 (bases 1 to 92171)
 AUTHORS Waterston,R.H.
 TITLE Direct Submission
 JOURNAL Submitted (12-JUN-1998) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 4 (bases 1 to 92171)
 REFERENCE 4
 AUTHORS Waterston,R.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-1999) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT

On Feb 24, 1999 this sequence version replaced gi:3213073.

SUBMITTED BY: WUGSC
Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

SOURCE INFORMATION:

This clone was derived from human PAC library RPC1-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.

VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is DJ0901A04, 200 bp overlap.
Actual start of this clone is at base position 1 of DJ0903G02;
actual end is at 92171 of DJ0903G02.

The location of this clone is unknown.

FEATURES

source

Location/Qualifiers

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/chromosome="unknown"
/clone_1ib="RPC1-5"
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repeat_region
488..796
/rpt_family="Alu"
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1029..1151
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repeat_region
1167..1625
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1848..2014
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misc_feature
2048..2173
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repeat_region
2230..2308
/rpt_family="Mariner"
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2745..3065
/note="match to EST AA574129 (NID:g2348644) ng51f03.s1"
misc_feature
3352..3739
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5403..5550
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7858..8160
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repeat_region
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/note="match to EST T84729 (NID:g713081) yd54b06.r1"
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14291..14468
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repeat_region
14587..14708
/rpt_family="purine-rich"
repeat_region
14818..15182
/rpt_family="Retroviral"
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15149..15623
/note="similar to EST A1275423 (NID:g3897697) q168e06.x1"
misc_feature
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Qy	18302	gttttgtaaatgtcgtttaagttcaatttggtctaaagtcagtttaagtcagtgttct	18361
Db	22229	ATTCTGAATAATATCTGTTAGGTCATTTGGTCTTAAAGTCACACTTTAAATCTAATGTTTCT	22288
Qy	18362	ttgtctgattccttgctctagatgacatcgtctcaatgctcgttaagtggggtgttgaaatttcaac	18421
Db	22289	TGTGTGATTTTATGCTCTGATGATGAACGTGTCACATGCTGACAGTAGGATATTGAAGTTCGA	22348
Qy	18422	act---attgtgttcagtgatcctcttcttctttagtgctagcagaactgttttagact	18478
Db	22349	ACTATCATTTGTTATTTGAGACTCTACTCTCCCTTATGATTTTAAATAATTTGCTATGTGT	22408
Qy	18479	cttagtaactccagtggttcgggtgtgcaatatgatattagaaattgtatatacttcgtgaa	18538
Db	22409	CTGGATGCACTGCTGTGGTTGCAATGCA--TATTTAGAATTTGTAATATTGTTGCTGAA	22466
Qy	18539	tttggtcctttaatatattataagacacttcttagtcctttttttttttttaaactgtt	18598
Db	22467	TTTATCCCTTTTATTTGCAATATATATACCTCTTGTTCCTTTTACAGATTTTGA---CT	22522
Qy	18599	tttagatggtttttctctcttgccatttttaggaattcaactctcacttttgaactcagaag	18658
Db	22523	TAAAGTCGTTTATATCTGATGATGAAGTTTAAAGCTACCTGATTACTTTGATTTCTGTTTG	22582
Qy	18659	tctgt 18662	
Db	22583	CGTG 22586	

	H513062	152077 bp	DNA	PRI	23-NOV-1989
Locus	Human DNA sequence from PAC 130G2 on chromosome 6p22.2-22.3.				
Definition	Contains ribosomal protein L29 pseudogene, ESTs and STS.				
Accession	AL008627				
Version	AL008627.1 GI:2769539				
Keywords	60S ribosomal; 6p22.2-22.3; L29.				
Source	human.				
Organism	Homo sapiens				
Reference	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Mammalia;				
Authors	Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
Title	Phillips, S.				
JourNameL	Direct Submission Submitted (02-JAN-1998) Chromosome 6 Project Group (http://www.sanger.ac.uk/HGP/Chr6/) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humandigest@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jan 13, 1998 this sequence version replaced gi:12578053. IMPORTANT: This sequence is the entire insert of clone 130G2. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above. This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre chromosome 6 mapping group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6/				
Comment	This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The true left end of clone 130G2 is at 1'yn this sequence. The true right end of clone 130G2 is at 152077. 130G2 is from the library RPLC1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ .				

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      /chromosome="6"
      /map="6p22.2-22.3"
      /clone="RP1-130G3"
      /clone_1bp="RPC1-1"
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      425. .458
      /note="17 copies of 2 mer 97 % conserved"
      4098. .4398
      /note="AluSx repeat: matches 302. .2 of consensus"
      5392. .5501
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      5547. .5848
      /note="AluSq repeat: matches 302. .1 of consensus"
      8419. .8536
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      /note="MIR2 repeat: matches 146. .23 of consensus"
      8556. .8643
      repeat_region
      /note="44 copies of 2 mer 91 % conserved"
      9351. .9486
      repeat_region
      /note="MIR repeat: matches 117. .256 of consensus"
      9897. .9923
      /note="9 copies of 3 mer 93 % conserved"
      9934. .10234
      repeat_region
      /note="AluJo repeat: matches 1. .298 of consensus"
      10241. .10541
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      /note="AluSg repeat: matches 1. .300 of consensus"
      11540. .11729
      repeat_region
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      repeat_region
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      12974. .130234
      /note="match: genomic DNAs B34759 279159"
      13227. .13338
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      /note="MIR repeat: matches 166. .48 of consensus"
      13728. .14019
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      /note="MER3 repeat: matches 16. .199 of consensus"
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      /note="AluJo repeat: matches 300. .1 of consensus"
      14997. .15096
      repeat_region
      /note="MIR2 repeat: matches 25. .138 of consensus"
      16165. .16714
      repeat_region
      /note="MER7B repeat: matches 1. .558 of consensus"
      16723. .17020
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      /note="AluSp repeat: matches 1. .303 of consensus"
      17047. .17677
      repeat_region
      /note="MER7B repeat: matches 558. .1203 of consensus"
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      R61223 AA513216"
      20113. .20755
      prim_transcript
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      complement(20536. .21038)
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      21004. .21078
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      /note="MER5B repeat: matches 172. .96 of consensus"
      complement(21079. .21274)
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      /note="match: genomic DNA Z84499"
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      /note="MER5B repeat: matches 123. .1 of consensus"
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repeat_region	/note="L1p2 repeat: matches 891. .1 of consensus" 39947. .40655
repeat_region	/note="L1 repeat: matches 5390. .4684 of consensus" 40656. .44689
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repeat_region	/note="MER25 repeat: matches 2136. .1177 of consensus" 45304. .45764
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repeat_region	/note="MIR repeat: matches 46. .251 of consensus" 47169. .47461
repeat_region	/note="AluDb repeat: matches 1. .302 of consensus" 47497. .47674
repeat_region	/note="ML1D repeat: matches 4. .169 of consensus" 47697. .47948
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repeat_region	/note="MER4B repeat: matches 284. .532 of consensus" 49741. .50223
repeat_region	/note="ML1TCB repeat: matches 501. .1 of consensus" 52697. .52762
repeat_region	/note="MIR repeat: matches 137. .73 of consensus" 52851. .53032
repeat_region	/note="L1M6 repeat: matches 902. .1045 of consensus" 53192. .53338
repeat_region	/note="L1M2 repeat: matches 710. .666 of consensus" 53204. .53238
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	repeat_region	/note="LORI repeat: matches 259. .1 of consensus"	
	repeat_region	58390. .58684	
	repeat_region	/note="AluJo repeat: matches 1. .294 of consensus"	
	repeat_region	58925. .59124	
	repeat_region	/note="MLTIF repeat: matches 541. .307 of consensus"	
	repeat_region	59122. .59381	
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Best Local Similarity	61.7%;	Pred. No.3,1e-192;	
Matches 2610; Conservative	0; Mismatches 1410; Indels 208; Gaps 33;		
QY	14582 cctgaattcatctcttgtaatgctcgtgaatagatattccattgtaataataaccacattt	14641	
DB	39518 CATGAACATCATTTTATATGGCTGATACATATCCATGAGGTATATGTCACATTTT	39577	
QY	14662 ctttcctgttcatccattgataagacacttaagtttgcatactcttgccgttgtaa	14701	
DB	39578 CTTAATCCAGTGTATCATTTGTTGGACATTGGGTGGTCCAAAGCTTGTGATTGTGA	39637	
QY	14702 tagctcctcagtaaacatactgctgcacatacttt-tagatatataattcttcttc	14760	
DB	39638 TAGTGTTCATTAACATACATACGCTGATGCTCTTTATAGCAGCATATTATAGCTCT	39697	
QY	14761 ttctgaaaaatcagtagtggaatgtgtcctagatgtaaaatagttctattttaactctg	14820	
DB	39698 TGGGTATATACCCATTAATGAGATGGATGGCTGGGTCAATGGTATTCTAGTTATAGATCCCT	39757	
QY	14821 gagaatctcactactgltttccatagagagctgtactaattacattccaccacatgta	14880	
DB	39758 GAGGATGGCCACATGATCTCCACAATGGTGAAGTATGATACGATCCACACACAGTG	39817	
QY	14881 tataagagttcccttttttccatagataaccaaa-----tgctgcgtctttaat	14933	
DB	39818 TAAAGTGTCCTATTTCTCCACATCTCTCCAGACACTCTGTTTCCGACTTTTAT	39877	
QY	14934 aaaaacattcgcataagataagtgatcatccattgtaattgattgattcattctct	14993	
DB	39878 GATTGCCATTCTAATGTGGTGAAGATGATGATCTCATTTGGTATTGCAATTTCTCT	39937	
QY	14994 tatgcctgtaattgttgagcaatttttccataaacctgttg-----ggtatgctt	15045	
DB	39938 GATGCCAGTATGATGTGAGCATTTTTCATGTTTTCGTTCGTGATTAATGTCTTCTT	39997	
QY	15046 tgaaaaagtctatcatcagtggtgttgccactttttaaagatattgttagatttttbg	15105	
DB	39998 TGAGGAGTCTGTTTCATGTTTTCGCCACCTTTTGTGATGGGGGTGTTGTTTTC	40055	
QY	15106 ttgttgaaatcgttgatctcctgtgtgtagtcggaatagtcacctggttgatgaataa	15165	
DB	40056 TTGTAATTTGTTTATGTTCAATTTGATATTCGATATTAGACCTTTGTCAATGATGAG	40115	
QY	15166 tttagaagatattctgtcatcacaagagattgtgtctcttccaaatcgttatctctt	15225	
DB	40116 GTTGTGAATAATTTCTCCCATTTGTGTAG-TTGCTGTGTCACATCGANGTGTTCTTT	40174	
QY	15226 tgcctatgcagaagctttttagtattatagagcccaattgtctgt-----	15272	
DB	40175 TGCTGTGAGGAGCTCTTATGTTTAACTAGATCCCATTTGTCAATTTGGCTTTGTTGC	40234	
QY	15272 -----	15272	
DB	40235 CATTCGTTTGGTATTTAGACATGAAGTCCTTGCCCATGCTATGTCTGAATGGTAA	40294	
QY	15272 -----ttctagatcttataagttttgggtcttcaactaaagcttcaatcca	15319	

[illegible][illegible]


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repeat_region 18491. .18567
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repeat_region 22549. .22838
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repeat_region 31887. .32030
/note="3 copies 48 mer 81% conserved"
repeat_region 31959. .32026
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repeat_region 32883. .32943
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repeat_region 33321. .34232
/note="LIR16 repeat: matches 57. .356 of consensus"
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repeat_region 36994. .37059
/note="L2 repeat: matches 2642. .2709 of consensus"
misc_feature 37933. .38313
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repeat_region 44272. .44530
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repeat_region 44560. .45371
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/note="LM2 repeat: matches 592. .744 of consensus"
repeat_region 45529. .45753
/note="LIP2 repeat: matches 5923. .6155 of consensus"
repeat_region 45768. .45921
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repeat_region 48694. .50660
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repeat_region 50661. .51079
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repeat_region 51080. .52340
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Best Local Similarity 63.8%; Pred. No. 1e-191;
Matches 2710; Conservative 0; Mismatches 1052; Indels 486; Gaps 37;

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DEFINITION	AC008886		HTG	03-AUG-1999	
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PROGRESS	***, 20 unordered pieces.				

ACCESSION	AC008886
VERSION	AC008886.1
KEYWORDS	HTG; HTGS_PHA8E1.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	1 (bases 1 to 94220)
TITLE	DOE Joint Genome Institute.
JOURNAL	Sequencing of Human Chromosome 5
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 94220)
TITLE	DOE Joint Genome Institute.
JOURNAL	Direct Submission
COMMENT	Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA www.jgi.doe.gov.

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*
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
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*			gap of unknown length
*	720	1561:	contig of 842 bp in length
*			gap of unknown length
*	1562	2552:	contig of 991 bp in length
*			gap of unknown length
*	2553	4021:	contig of 1469 bp in length
*			gap of unknown length
*	4022	6364:	contig of 2343 bp in length
*			gap of unknown length
*	6365	7026:	contig of 662 bp in length

	*	7027	9459:	contig of 2433 bp in length	
	*			gap of unknown length	
	*	9460	11038:	contig of 1579 bp in length	
	*			gap of unknown length	
	*	11039	12945:	contig of 1907 bp in length	
	*			gap of unknown length	
	*	12946	15100:	contig of 2155 bp in length	
	*			gap of unknown length	
	*	15101	16805:	contig of 1705 bp in length	
	*			gap of unknown length	
	*	16806	19103:	contig of 2298 bp in length	
	*			gap of unknown length	
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Best Local Similarity		63.4%;	Pred. No. 3./e-18;		
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Db	64970	TATCATTAAGTCCACTGATGAAACAATTAGTGATTCATATTTGGCTATCAGAATAG	64911		
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Oy	14938	gacattcgtacatgataagtgatatctcatcttgaaattgattgcatttccattia	14997		
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 Qy 18007 acatttcttctgttctcaaaaacttttcttaattctctgcttaattcttctatgacc 18066
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 DEFINITION
 AC000385
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 VERSION
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 SOURCE
 ORGANISM
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 Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homiinae; Homo.
 REFERENCE
 1 (bases 1 to 165491)
 Evans,G.A., Athanasiou,M., Basit,M., Bradbury,P., Brignac,S.,
 Bumester,R., Davis,C., English,C., Franklin,T.L., Garner,H.R.,
 Gee,V., Gordon,M., Gotway,G., Grant,O., Hamner,J., Harris,J.,
 Hinson,S., Narayanaswamy,U., Newton,J., O'Brien,K., Patel,P.,
 Schageman,J., Schilling,P., Schultz,R., Syed,M., Valenzuela,D.,
 Ward,T. and Wilson,R.
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 unpublished
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 2 (bases 1 to 165491)
 Evans,G.A., Bradbury,P., Brignac,S., Bumester,R., Burbee,D.,
 Davie,J., Davies,C.J., Davis,C., English,C., Fondon,T.,
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 Hamner,J., Harris,J., Hinson,S., Megarity,C., Narayanaswamy,U.,
 Newton,J., O'Brien,K., Oliver,T., Patel,P., Probst,S., Rayner,S.,
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 Ward,T. and Wilson,R.
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Direct Submission
 Submitted (04-APR-1997) Genome Science and Technology Center,
 University of Texas Southwestern Medical Center at Dallas, 5323
 Harry Hines Blvd, Dallas, TX 75235-8591, USA
 REFERENCE
 3 (bases 1 to 165491)
 Evans,G.A., Athanasiou,M., Basit,M., Bradbury,P., Brignac,S.,

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DEFINITION	Human DNA sequence from cosmid L96A2, Huntington's Disease Region,		PRI
VERSION	chromosome 4p16.3, containing multiple EST matches defining gene		23-NOV-1999
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SOURCE	Z68165		
ORGANISM	268165.1 GI:1107693		
REFERENCE	4p16.3; Cpg island; Gene fragment.		
AUTHORS	human.		
TITLE	Hum sapiens		
JOURNAL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
COMMENT	Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
	1 (bases 1 to 35281)		
	Williamson,H.		
	Direct Submission		
	Submitted (04-DEC-1995) Sanger Centre, Hinxton, Cambridgeshire,		
	CB10 1RQ, England. E-mail enquires: humpub@sanger.ac.uk		
	IMPORTANT:		
	The true left end of clone L96A2 is at 1 in this sequence. The true		
	left end of clone L19H1 is at 35182 in this sequence. The true		
	right end of clone L27H9 is at 8050.		
	The start of this sequence overlaps with the end of clone L27H9.		
	This sequence is not the entire insert of clone L96A2. It may be		
	shorter because we only sequence overlapping sections once, or		
	longer because we arrange for a small overlap between neighbouring		
	submissions.		
	This sequence has been finished according to sequence map criteria		
	as follows. An attempt is made to resolve all sequencing problems,		
	such as compressions and repeats, but not necessarily within known		
	annotated human repeat sequence elements (e.g. Alu). Where the		
	sequence is ambiguous, there is an annotation using the 'unseq'		
	feature key.		
	L96A2 is from cosmid library LA0NCO1 constructed at the Human		
	Genome Center, Los Alamos National Laboratory, NM 87545 under the		
	auspices of the U.S. Department of Energy. The library was		
	constructed using flow-sorted human chromosome 4 from a		
	Hamster-Human hybrid cell line (UV20HL21-27) containing human		
	chromosomes 4, 8 and 21.		
	VECTOR: SCOS+1		
	L96A2 is contained in a clone contig spanning		
	2M which is described in Baxendale et al, Nature Genetics 4 (1993)		
) 181-186. See also Myers et al, Cytogenet Cell Genet. 66 (1994		
) 218-230.		
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	/db_xref="taxon:9606"		

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ORIGIN
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Matches 2628; Conservative 0; Mismatches 1225; Indels 344; Gaps 35;
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Oy	18552	tattataacgaactctcttagtctcttttttttttttaacigtcttttagatgcttt	18611
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DEFINITION	Homo sapiens clone NH027118, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
ACCESSION	AC009408
VERSION	AC009408.2 GI:5923732
KEYWORDS	HTG; HTGS_PHASE1.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE 1 (bases 1 to 171212)
AUTHORS Waterston, R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 171212)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (21-AUG-1999) Genome Sequencing Center, Washington

COMMENT

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On Sep 25, 1999 this sequence version replaced g1:5757530.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
*      1      3801: contig of 3801 bp in length
*      3802      3819: gap of unknown length
*      3820      3360: contig of 29341 bp in length
*      3361      33378: gap of unknown length
*      33379      171212: contig of 137834 bp in length.

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FEATURES	Location/Qualifiers
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[illegible]

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Best Local Similarity	67.0%	Pred. No. 7.4e-184:		
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Db 456

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Dh 45571	CTCGAACCTCTCAACTCTCTGGGTTCAAAGCAATTCTACGTCCCTCAACCTCCGGAATACTGG	45512
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Dh 45511	GACTCAAGGCCCAACACACCACTGATCTTAATTTTT-----TGATTTTTTAGGAG	45461

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Db 45310 TGGCTGGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACTGTCCTCCACCGTTACT 45311

Db 45340 AATTTTGACATTGATTTTGTGATTAACCACTTACTGAATTCATCATCAGTTCCTAA 45281

Db 45280 CAGTTTTTACIGGAGCCTTTAGGATTTTAAATAATATGATCAAGTGTTCGAACACAG 45221


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Db 44712 AGATCTTAGTGAAGAGCTTTCAATTTTCCCTGTTCTGATTAACATTAAGTGAAGTTT 44653
Qy 16950 atcataatgagccttatacttctgaagtgatcctctctcgtcctcctcctcctcctcctc 17009
Db 44652 GTCAATATAGCCTTATATGTTTGAAGTACATTTCTTGTAACCTGATTTGTTGAGAGT 44593
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Qy 17070 catatgcttctgcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 17129
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Qy 17130 gttaacatcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 17189
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Qy 17190 gatttgcgttggaattcgttctcgtatattcgttgcgaatttgcattcgttgcatt 17249
Db 44414 GATGTGCTGTTGATGCTAGTCTAGTATTTGTTGAGATTTTTCATCTATGCTATG 44385
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Fri Mar 3 12:08:41 2000

us-09-339-352-9.rge

Page 52

Qy 18553 attataaacgacttccttagtcctttttttttaactgtttttagatgtttt 18612
| | | | | | | | | | | | | | | | | |
Db 43083 AATACATAATGGCTTCCTTTTGTGCAATTCATTAAAGTCTAT 43024

QY	18613	tct	18615
Db	43023	TTT	43021

Search completed: March 2, 2000, 21:20:13
Job time: 295484 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 3, 2000, 04:59:16 ; Search time 8603.19 seconds

(without alignments)
-6776.743 Million cell updates/sec

Title: US-09-339-352-10_COPY_15000_34200

Perfect score: 19201

Sequence: 1 agcacatcctcctcctcctc.....taccaccttagtccacga 19201

Scoring table: IDENTITY_NUC

Searched: 821193 seqs, -1518192014 residues

Database: GenEmbl:*

Word size: 0

Number of hits that pass the threshold: 1642386

1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_pal:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_pl3:*
10: gb_pr2:*
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45: gb_hcg14:*
46: gb_hcg15:*
47: gb_hcg16:*
48: gb_hcg17:*
49: gb_hcg18:*

50: gb_pl3:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	19201	100.0	128230	11	HS313L4	299943 Human DNA s
2	950.4	4.9	115218	10	HS159A1	AL034397 Human DNA
3	883.6	4.6	166182	33	CNS01DU	AL133241 Homo sapi
4	868.6	4.5	153781	33	HS01689C5	AL118803 Homo sapi
5	846.2	4.4	30110	11	HS124H12	249918 Human DNA s
6	836.6	4.4	153661	11	HS399M14	296074 Human DNA s
7	830.8	4.3	154269	41	AC011350	AC004704 Homo sapi
8	824.8	4.3	134187	40	AC004704	AC004704 Homo sapi
9	821.6	4.3	99036	40	AC005773	AC005773 Homo sapi
10	804	4.2	96558	11	HS598A24	AL031115 Human DNA
11	804	4.2	61187	11	HS8316	299130 Human DNA s
12	797.4	4.2	104594	11	HS0390L14	AL049550 Human DNA
13	751.6	3.9	111994	11	HS296K21	283821 Human DNA s
14	751.6	3.9	114173	11	HS884M20	AL020591 Homo sapi
15	731	3.8	143376	42	AC012272	AC012272 Homo sapi
16	709.8	3.7	167899	44	AC012027	AC012027 Homo sapi
17	707.6	3.7	84464	11	HS782D21	AL022399 Human DNA
18	701.4	3.7	155960	11	HS288M22	AL035467 Human DNA
19	700.6	3.6	151895	42	AC010142	AC010142 Homo sapi
20	695.4	3.6	93481	40	AF201337	AF201337 Homo sapi
21	691.2	3.6	195960	44	AC013569	AC013569 Homo sapi
22	690	3.6	153428	44	AC015459	AC015459 Homo sapi
23	687.8	3.6	209613	40	AC005539	AC005539 Homo sapi
24	679.2	3.5	130252	44	AC015631	AC015631 Homo sapi
25	674.4	3.5	139515	11	HS38C16	AL035604 Human DNA
26	673.4	3.5	161580	40	HUAC002307	AC002307 Homo sapi
27	673	3.5	39706	11	AC000073	AC000073 Homo sapi
28	672.6	3.5	219580	32	HS455H15	AL078590 Homo sapi
29	672.2	3.5	36955	10	AP000543	AP000543 Homo sapi
30	669	3.5	38993	10	AP000544	AP000544 Homo sapi
31	667.4	3.5	169424	42	AC011961	AC011961 Homo sapi
32	664.2	3.5	100152	40	AC000085	AC000085 Homo sapi
33	662.6	3.5	162473	42	AC012009	AC012009 Homo sapi
34	662.6	3.5	186834	42	AC012082	AC012082 Homo sapi
35	660.2	3.4	178361	40	AC006042	AC006042 Homo sapi
36	656.4	3.4	111648	10	HS16C2	AL049911 Homo sapi
37	654.2	3.4	161973	10	HUAC002038	AC002038 Homo sapi
38	650.6	3.4	326663	40	AF011889	AF011889 Human Xq2
39	650.6	3.4	171801	41	AC009808	AC009808 Homo sapi
40	649.6	3.4	124645	11	HUAC004638	AC004638 Homo sapi
41	644.8	3.4	153060	33	AC007780	AC007780 Homo sapi
42	642.6	3.3	136222	33	AC006477	AC006477 Homo sapi
43	641	3.3	171831	44	AC016706	AC016706 Homo sapi
44	640	3.3	210680	44	AC013530	AC013530 Homo sapi
45	635.8	3.3	135886	10	HSX15T2	U80460 Human Xq13

ALIGNMENTS

RESULT 1
LOCUS HS313L4
DEFINITION Human DNA sequence from PAC 313L4 on chromosome 1q24. Contains
ACCESSION Z99943
VERSION Z99943.1 GI:2887308
KEYWORDS 1q24.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 128230)
AUTHORS Pearce,A.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1997) Chromosome 1 Project Group
(http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clonerequest@sanger.ac.uk
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 14, 1998 this sequence version replaced g1:2578084.
IMPORTANT: This sequence is the entire insert of clone 313L4.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variations annotated may not be found in the sequence submission
corresponding to the overlapping clone as we submit sequences with
only a small overlap as described above.
This sequence was generated from part of bacterial clone contigs of
human chromosome 1, constructed by the Sanger Centre chromosome 1
mapping group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1/
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu) where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The true left end of clone 313L4 is at 1 in this sequence. The true
left end of clone 295C6 is at 122337.
The true right end of clone 313L4 is at 128230.
313L4 is from the library RPCI1 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/
Location/Qualifiers
1. 128230
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/chromosome="1"
/map="1q24"
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/clone_1kb="RPCI-1"
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1600. .1760
/note="AluSx repeat: matches 277. .121 of consensus;
incomplete repeat"
1781. .2080
/note="AluSg repeat: matches 300. .2 of consensus"
2081. .2210
/note="AluSx repeat: matches 136. .3 of consensus;
incomplete repeat"
2692. .2780
/note="MIR2 repeat: matches 44. .139 of consensus"
3140. .3212
/note="MIR2 repeat: matches 146. .66 of consensus"
4164. .4333
/note="AluSg repeat: matches 300. .130 of consensus;
incomplete repeat"
4334. .4625
/note="AluSg repeat: matches 303. .1 of consensus"
4630. .4669
/note="20 copies of 2 mer 88 & conserved"
4672. .4804
/note="AluSg repeat: matches 133. .1 of consensus;
incomplete repeat"
5281. .5588
/note="AluSx repeat: matches 1. .302 of consensus"
6070. .6291
/note="MIR repeat: matches 250. .1 of consensus"
6575. .6865
/note="AluSx repeat: matches 301. .11 of consensus"
7450. .7732
/note="AluSx repeat: matches 1. .281 of consensus;
incomplete repeat"
7732. .8034

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8082. .8166
repeat_region /note="FLAM_C repeat: matches 49. .133 of consensus"
8605. .8710
/note="AluO repeat: matches 190. .302 of consensus;
incomplete repeat"
8735. .8909
/note="FM repeat: matches 175. .4 of consensus"
8914. .9169
/note="AluSp repeat: matches 302. .36 of consensus;
incomplete repeat"
9271. .9759
/note="MUT2_internal repeat: matches 1795. .1306 of
consensus"
9760. .10052
/note="AluSx repeat: matches 1. .296 of consensus"
10053. .10213
/note="AluO repeat: matches 134. .296 of consensus;
incomplete repeat"
10272. .10571
/note="AluY repeat: matches 1. .300 of consensus"
10573. .11108
/note="MUT2_internal repeat: matches 1264. .725 of
consensus"
11111. .11754
/note="MUT2_internal repeat: matches 667. .1 of consensus"
11751. .11789
/note="MUT2 repeat: matches 391. .353 of consensus"
11876. .12153
/note="MUT2FB repeat: matches 348. .70 of consensus"
14223. .14520
/note="AluY repeat: matches 301. .1 of consensus"
14796. .15232
/note="MSY1 repeat: matches 1. .426 of consensus"
15237. .15539
/note="AluSx repeat: matches 301. .1 of consensus"
15550. .15629
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mer 86 & conserved"
15666. .15723
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17316. .17618
/note="AluY repeat: matches 300. .1 of consensus"
17628. .17921
/note="AluSx repeat: matches 300. .1 of consensus"
18048. .18339
/note="AluY repeat: matches 1. .292 of consensus"
18346. .18599
/note="AluSx repeat: matches 39. .300 of consensus;
incomplete repeat"
18849. .19511
/note="LI repeat: matches 5228. .4535 of consensus"
19512. .19802
/note="AluSc repeat: matches 294. .1 of consensus"
19803. .20374
/note="LI repeat: matches 4539. .3971 of consensus"
20381. .20513
/note="MIR repeat: matches 225. .82 of consensus"
20699. .21000
/note="AluSg repeat: matches 1. .303 of consensus"
23516. .23790
/note="AluY repeat: matches 302. .32 of consensus;
incomplete repeat"
24031. .24436
/note="LMB6 repeat: matches 922. .492 of consensus"
24433. .24828
/note="LMB6 repeat: matches 417. .1 of consensus"
24699. .25097
/note="LI repeat: matches 5384. .4957 of consensus"
25146. .25252
/note="LIP11 repeat: matches 594. .489 of consensus"
26389. .26467
/note="MIR42c repeat: matches 1537. .1457 of consensus"

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	repeat_region	26799..27525	/note="MER42C repeat: matches 1466..720 of consensus"
	repeat_region	27686..27987	/note="AlusX repeat: matches 2..302 of consensus"
	repeat_region	29924..30226	/note="Alusx repeat: matches 299..1 of consensus"
	repeat_region	30296..30594	/note="Alusx repeat: matches 301..2 of consensus"
	repeat_region	31058..31167	/note="MER5B repeat: matches 31..134 of consensus"
	repeat_region	31174..31438	/note="LIMC1 repeat: matches 1064..787 of consensus"
	repeat_region	32457..32723	/note="Alub repeat: matches 294..1 of consensus"
	repeat_region	32727..32750	/note="12 copies of 2 mer 100 & conserved"
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	repeat_region	33035..33141	/note="MIR2 repeat: matches 139..36 of consensus"
	repeat_region	34165..34469	/note="AlusX repeat: matches 1..300 of consensus"
	repeat_region	36498..36799	/note="Aluy repeat: matches 301..1 of consensus"
	misc_feature	complement(36864..37172)	/note="match: 253371 STS containing (CA) repeat"
	repeat_region	37045..37090	/note="23 copies of TG 100 & conserved; differs from 253371"
	repeat_region	38392..38604	/note="MER20 repeat: matches 2..218 of consensus"
	prim_transcript	<38614..>73039	/note="match: multiple ESTs; match: R05711 H29257 T90778 H08848; match: R64027 R39393 AA291124"
	repeat_region	39530..39817	/note="AlusX repeat: matches 1..303 of consensus"
	repeat_region	41025..41616	/note="LIMC2 repeat: matches 479..1075 of consensus"
	repeat_region	42884..42782	/note="MIR repeat: matches 126..227 of consensus"
	repeat_region	45318..45478	/note="MIR repeat: matches 20..194 of consensus"
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	Best Local Similarity	100.0%; Pred. Mismatches 0; Indels 0; Gaps 0;	
	Matches 19201; Conservative	0; N/A	
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Dy	61	ttcaccttgcacatgatgtttaagtcttctcctaaggctccccagaagcggaacaatgc	120
Db	15060	TTCACCTTCTGCATGATTGAATTCTCTGAGGCGCTCCACAGAAGCGGACAATGSCA	15119
Dy	121	gcatacgtctccgtgtgtagcgtcagaaccagcagccaattaaactctttctctaata	180
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Dy	181	aattaccagctcgaagatctcttctaataagtgatagatatgacacatacataat	240
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Dy	241	tgtttttcggagtttttttgaagagaggtctcactcgtcaccggcgctgtagtacgtg	300
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Dy	301	cctaaccttgtcactcagcgaacctccacctcgaagttcagaagcattctccacctcagtc	360
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QY	361	tcgcagatgctcgggagcccaagctgcaccccaatgcccagaatgccttggtgttttt	420
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QY	421	ggtagagaaagggttcacacatgttagtaacatgctgtcttgagccctgaactaagtta	480
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QY	481	tcctgcctccttagccttaccaagtgctggaataagtgtygaaccaactgcaccagcc	540
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QY	541	aaagggaactaatacatacaacatacatatatacatatatacatatatatacatat	600
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QY	841	gtaatttacctatcacagatgtaagaatgaagctcacaagctcctgtaatgtgtcgtcctt	900
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QY	901	cccatataaatataaatatgccaatgacaccccgaaagaagcccgaggagcctgtgtaagag	960
Db	15900	CCCATATAAATTAACATTTGCCATGACACCCGAAAGGCCCGAGGAGCGTGTATAGCAG	15959
QY	961	ccataaccctggggaatatagctagaagaactttgtctgcgcccaactcacaagctgt	1020
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QY	1021	ctggattgcccctcaatattgtcatataccctgtttaactaagtcacactccaacatct	1080
Db	16020	CTGGATTTCCCCCTCATATTGTGCATATCCCTGTAACTACAAGTCACTCACTCAAAACATCT	16079
QY	1081	actttgagctctcttcccttaacccctctatctgcgtccagaactcctcttaccgaaaaatgta	1140
Db	16080	ACTTTGGCTCTTCTTCCTTAACCCCTTATATGCTGCAGAACCTCCTTACCAAAAAATGTA	16139
QY	1141	gcaactccacaactcttttcccaaccttcaagacacataacctttatagttcacatga	1200
Db	16140	GCAACTCCCAATCTTTTCCACCCCTTCAAGACCATATCCTTTATATGTTTCACTACGA	16199
QY	1201	caagttctcagagctcatcaagctcttcccatccctccctcgtctttgttctgtatccgttac	1260
Db	16200	CAGTTTCTGGAGCTCATCAAGTCTTCCCATCCCTCCCGCTTTGTTTGTATTCGTTAC	16259
QY	1261	ttccctgagctcttccctctccgcgtccaaactgtgaagtcatagttcattggtataatcat	1320
Db	16260	TTCCCTGAGCTCTCCCTCTCCCGCTCAAACTTGAGTGCATATGTTATATATATCAT	16319
QY	1321	tcctcttgaagaagctccctacttcccagaagcctctcgtgcacatcatgtaacttaactgca	1380
Db	16320	TCCCTTGTAAAGGCTCTACTTCCCAACCCCTTCTGTGCCATCATTTGCACTTACCTGCA	16379
QY	1381	atccctcaaacctctgggaaaaacctacaactctcttttcaatcccttaagaacattgtgtctt	1440
Db	16380	ATCCCTCAACCTCTGGGAAAAACCTCACTATCTCTTTTATCATTCCTTAAGCATTTGTGCTT	16439
QY	1441	taattatgtccctcttagatcatcttactactacaataaacaatgagctagaatttctca	1500

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QY 1501 tcttaaaacccctctcttggtctatagtcctctttagctacattctctggcgctaacctc 1560
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QY 1561 tttagcaatttttacaanaatagactatacctctctcttgtagtgaacccctctctc 1620
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QY 1621 cactctctctgctcagccacccaccagctgctctgcccacttccaatgaaactctctcta 1680
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QY 1681 tcagagatcaccaagagagactccaaggttgacaacacatatagttcttccctataagcaact 1740
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OY	18660	TATAACAAGTATAAAGATGATACCGCTTAACATATATATATAGGCGAGATACCTTATATGATAC	18719
OY	3721	ttccaataaaagaatactctccaactttaaaataacatacatagatgcctgaag	3780
Db	18720	TTTCAATATAAAAGATATCTTCCCACTTTTAAATATATATATGAGATGCCGAGGG	18779
OY	3781	aattcctaaggagatcacaatgatacagatacacaataacagaalaggaaactaag	3840
Db	18780	AATTCTTAAGAGAGTCACATAGCTATCATCATCACTACCTATACCAATATCGAATAGCAACTATAG	18839
OY	3841	tttatcttgaaatggaatctgtaagaattttctctcaactcctgagatgtctgttactctg	3900
Db	18840	TTTATTTTGGATGGATGTGTGAAGATTTTCTCTCACTCTGTGGTTGTCTGTATCTCTG	18899
OY	3901	ctgaactgtctcttttgcacacacaaaagcctttaagtttaagtcccaagctattatcttg	3960
Db	18900	CTGACTGTATCTTTTGCCACACAAAAGCTTTAGTTTAAAGTCCAGCATTTATCTGTG	18959
OY	3961	tttttgttgcaattgctctttgggtcttggtcaatgaagctttgcgttaagctaatgtcag	4020
Db	18960	TTTTTGTGCAATTCCTTTTGGGCTTGTGTATGAAGCTTTTGCCGTAAAGCTATATGTCAAG	19019
OY	4021	aagggttttccaaegttctctctccagaaattttaagttcaaggtctagaattcaagtc	4080
Db	19020	AAGGTTTTTCCAAATGTTCTCTCTTCAAGATTTTATAGTTTACGCTTATAGTTTAAATGTC	19079
OY	4081	cttgatactacttgagttgaattttgtataaagtgagaaatgaaatccagttcaactct	4140
Db	19080	CTTGTATCATCTTGTAGGTGATTTTGTATTAAGTATGAGATATGAGATCCAGATTATCTCT	19139
OY	4141	cctacaatggtgtagccaattttccacagacaaagtgttgaatgaaggtgctctcccca	4200
Db	19140	CCTACATGGGCTACCCACATTAATCCAGACAGATGTGAATPAGGGTCTTTTCCCA	19199
OY	4201	cttgatgtttttgtttgtctttgacaaatgaatcagatagcgttaagatattggtttatttt	4260
Db	19200	CTTGAATGTTTTTGTGTGCTTTGTTCATATGATCATGATGCGTAAAGTATTTGGGTTATTTT	19259
OY	4261	tgggtctctctatttgctcccttggtactatgtactatgtactatttataacagtlaccaggtctc	4320
Db	19260	TGGGTTCTCATATTTTGTCTTGTTCATATGATGCGCTATTTTATTAACATACATACAGGCTGC	19319
OY	4321	tttgaatgactgtagcctatagtaatgatttgaaatccagtaatgtagatctccagatcg	4380
Db	19320	TTTGAATGACTGGGCTTATATGATATGTTTGAATTCAGTAAATGTGATGTCTCCAGATTG	19379
OY	4381	tatgaaggtccttttttggttccataatgaatttgaattgtttttctagtctctgtga	4440
Db	19380	TATGACGAGCTCTTTTGGTTCCATATGAATTTTAGGATGTGTTTTTTCAGTTCTGTGA	19439
OY	4441	aactgatagtgataatttgatagtggaattgctgtgaatttgatagattactttgggaagat	4500
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OY	4501	catcatcttcaactttttttcttctctgagaagaagatcctgactgtctgcgacaggttgat	4560
Db	19500	CATCATTTTCACTTTTTTTTTTTCTTCGAGACAGAGTCTCGCTCTGTGCCAGGCTGGAT	19559
OY	4561	tgcgaatgctgatactcttgccgtactgcgaactctgctctctctgtgttcaagcaattctctct	4620
Db	19560	TGCATATGGCGTATATTTGCTTACATGCAACCTCTCCTCTCTGGTTTCAAGCAATTTCTCT	19619
OY	4621	gctcagacctcccaagtagctggaactcaagaagcgacatcaacgaagcccaagtaattttgta	4680
Db	19620	GCTCAGGCTCCCAAGTATGCTGGGACTACAGGCGCACATACAGCCACGATATTTTGTGA	19679
OY	4681	tttttaagtagaaggggatttcaacatgattagccaaggtgtgtctcgatactcttgacctcg	4740
Db	19680	TTTTTATAGTAAACGGGTTTATACCATATGTATACCAAGGCTGGTCTGTATCTTTGACCTCG	19739

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QY	4801	gacctgcgaattaaattcttcctcatcsgfyagagcayggatgtgttcctctgtctatg	4860
Db	19800	GCCTTGCATATTAAATTCTTCCATCCGTGAGCATGGATGTGTTCTTTGTGTTAAG	19855
QY	4861	tcaatcgtatcttcttcacgacgfygtccgtatgttccctgtagaagfygttcaacctc	4920
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QY	4921	ttggttaggtataatccctaagaattgttctaacttttttgcagctatctyagaaggg	4980
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QY	4981	ttgagfcttgaattbatacttcgaagcttggtgtcgtgtgtgtgtatagaagacacagat	5040
Db	19980	TTGAGTCTTGATTGTGATTCTCAGCTGGTGTGCTGTGGTGTATGAAGACCTACTGATT	20035
QY	5041	tgttacataatttctgcacccggaacgcgcgaattccttatacagctctcggagcttt	5100
Db	20040	TGTTTACATTAATTTTGCAATCTGGAACGCGTGAATCTTTATATCAGTCTCGGAGCTTT	20099
QY	5101	ctgagagagctcttaggygtttcttagytaaacagcttatacaacgaacaacaacag	5160
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QY	5161	ttgacctcctcttactgatttgatagcccttatcttctctctgtctgtattctcgg	5220
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Db	20220	GCTAGGACTTCCAAATTCCTTGTGTGAAGAGAAAGTGTGAAGTGGGACATCTTGCTCTATT	20277
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Db	20280	CCAGTCTCTAGAGGGAGCTGCTTCAACCTTTCCTATCATTAATTGTGTGGCTGTGGGT	20333
QY	5341	ttgtcatagatggtctttatatacatgtgagatgtaatgygaacagggcatcttaagccctt	5400
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QY	5401	acaaataataactcaatctatctctgttaataactcttgaagtcgctactattagaataa	5460
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QY	5521	ttctctgtctcgggfytaaccctgtgattcaatagatgtgcaagcaatagctcaacccggaa	5580
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QY	5581	gfttttcaggaaccccttcttagacatctgtttaaaaacttaaaaggggaacatttga	5640
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QY	5641	tgtgtaaaaaaactlaggaagcaltgltccagagctaaagfygttctttaaaccacaaaaaag	5700
Db	20640	TGTGTAAAACAATTAGGAAGCATGTGCCAAGTCTAAGTCTCTTTTAAAAACCAAAAAAAG	20699
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Db	20760	CACCTGAGTCAAGAGTGTGAACACCAAGCTGGCCAAACATGAGCAAAACCCCTGTCTCACTA	20811
QY	5821	aaaatacaaaaactlagtgggccaagfygtgtgtgctataatcccaagctacttgggaag	5880

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Q	10261	atttgagtttggaattacatccaatgatcatctgagcttgaagtgtttcatacc	10320
D	25260	ATTTGCGTTTGGAAATTATCTCMAAATGCACTTGGCTTGAAAGTTGTTATATCAC	25319
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D	25380	ATTTCAGAAACCCCTGGAAATTAAATCCAGTCTCTTGGGTAAAGACCCCAAGGAATTCAG	25439
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D	25440	ATATTTTCATTCATTAATGTTTACAGTAGTCAGGACMAAAGTTTCTTCAATTATC	25499
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D	25620	ATTGTGTCTGTGTATTAATCAAGTAGTAGTATTAACCTCAGCAATACAGGC	25679
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D	25680	AGCCAACCTCAGTAGATATTAATAATCCAGATATATGAACATATATAGTTCCTTGTTA	25739
Q	10741	aagagagagcttaagggaataatcttgaataacatacaacacttccatactgcagaagca	10800
D	25740	AAGAGAGGCTTAGGGGAAATCTTGAAATACATACACCTTCTTAACTCAGACAGCA	25799
Q	10801	tatttgccacatggagaaagtaacaaaagaagctatagaaagctaaagttagttatggca	10860
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D	25920	TTCCTAATTTTATACACTGTATCAAGTCAGTATATCAAAAAAGAACTTCACAAATTG	25979
Q	10981	tctaattctgttctcgttctctataatgatcttgataacctcaataagttaacttccctttt	11040
D	25980	TTTAAATCTGTGTTCTGTTCTGTATGATGTGGATACCTTCAATAAGTATCTTCTTTT	26039
Q	11041	tgggcttagagtaatttcacatctataaagtgaacgttaactagatgaatttccaagctata	11100
D	26040	TGGGCTAGAGTATTTTCACTATTAATAATGAACGTGAATGATGATTTCAAAGCTATA	26099
Q	11101	gtagaacaataataatagaggtgaataatagaagcttactactcgtgaagcaagctgcacaagca	11160
D	26100	GTAGAACAAATTATATAGAGGTGAATATAGAGCTACTACTGAGGAGCAAGCTGCAATCAGCA	26159
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Q	11221	aaagtccaataataatcatgagctgtgagacatctggcttagagcaaaatagtcgcataacc	11280
D	26220	AAAGTTCAAAATATATCATGCGCTGGAGACATCTGGCTAGAGACAAATATGTCGACATAC	26279
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[illegible]

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QY	12481	tgaactctggaacatcatctgtctccctaaacttcaactacatatactttcat	12540
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QY	12541	gaagcagaaggaaaaataatcatcttagtaagagtcacctcaaaatggctgtgattt	12600
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QY	12601	aaaaaataacttcaaggaaccttgagtagtcatcttgacagataatacatgtagaatta	12660
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QY	12901	agaagcttcagtagagccgagatgtgagacatctgcactccagccttggcgcgacagagagagac	12960
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QY	12961	tccatctcaaaaaaaaaaagaagaagaataaagtatgcaatactagtlttta	13020
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QY	13201	caataaatttccagtaattatctcaaatgctctcttcttccctcttttgtgtatc	13260
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QY	13502		
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Qy 18961 tatcaagtatcaagactcttgcgtgtacccaagaagaagaagatagtgtaagaagct 19020

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QY 19201 a 19201
Db 34200 A 34200
RESULT 2
HS159A1/c
LOCUS
DEFINITION
Human DNA sequence from clone 159A1 on chromosome Xq12-13.3.
Contains a novel gene and a Heterogenous Nuclear Ribonucleoprotein
G (HNRNP G, Glycoprotein P43) pseudogene. Contains ESTs, an STS,
GSSs, genomic marker DXS1213, and a ca repeat polymorphism,
complete sequence.
AL034397
ACCESSION
AL034397.1 GI:3980338
VERSION
HTG; ca repeat polymorphism; DXS1213; Glycoprotein P43;
KEYWORDS
Heterogenous Nuclear Ribonucleoprotein G; HNRNP G;
human.
SOURCE
HOMO sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 115218)
AUTHORS
Pearce, A.
TITLE
Direct Submission
JOURNAL
Submitted (04-DEC-1998) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
COMMENT
Requests: clonequest@sanger.ac.uk
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence is the entire insert of clone 159A1. This sequence
has been finished according to sequence map criteria as follows. An
attempt is made to resolve all sequencing problems, such as
compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key
This sequence was generated from part of bacterial clone contigs of
human chromosome X, constructed by the Sanger Centre Chromosome X
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/ChrX
159A1 is from the library RPc16 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/VECTOR: pPAC4.
FEATURES
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/map="q12-13.3"
/clone="RP6-159A1"
/clone_1b="RPc1-6"
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repeat_region
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repeat_region
1155..1214

/note="12 copies 5 mer aaat 95% conserved"
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2840..2940
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3146..3301
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4047..4162
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4439..4563
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4827..5188
/note="L1P29 repeat: matches 5455..5826 of consensus"
5386..5557
/note="86 copies 2 mer aa 58% conserved"
5728..5982
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6334..6493
/note="PRAM repeat: matches 9..173 of consensus"
6727..6932
/note="MIR repeat: matches 2..244 of consensus"
7748..8631
/note="L2 repeat: matches 1570..2525 of consensus"
8632..9160
/note="MUT1D repeat: matches 1..505 of consensus"
9161..9251
/note="L2 repeat: matches 2525..2609 of consensus"
9310..9415
/note="HAL1 repeat: matches 1499..1593 of consensus"
9699..9781
/note="L2 repeat: matches 2660..2742 of consensus"
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/note="MER63 repeat: matches 712..788 of consensus"
10335..10608
/note="L2 repeat: matches 2241..2529 of consensus"
10986..11053
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/note="complement(11001..11403)
/note="match: STS 224013; genomic marker DXS1213"
11066..11103
/note="19 copies 2 mer gt 100% conserved"
/note="complement(11067..11102)
/note="18 copies of ca 100% conserved; differs from
224013"
11546..11658
/note="MIR repeat: matches 57..172 of consensus"
11961..12094
/note="MIR repeat: matches 2..148 of consensus"
12196..12267
/note="MIR repeat: matches 151..226 of consensus"
12368..12482
/note="MIR repeat: matches 35..154 of consensus"
12706..12777
/note="36 copies 2 mer gt 86% conserved"
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AA972857 AA436814 R62969 W74268 H05057 N78991 AA813538
AA939378 AA627735 A1168499 R39812 R59136 R56602 D79546"
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TEKASVC"
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repeat_region 16537..17616
/note="24 copies 45 mer 55% conserved"
repeat_region 16655..17256
/note="301 copies 2 mer tt 55% conserved"
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/note="181 copies 5 mer ttat 55% conserved"
repeat_region 16709..17628
/note="40 copies 23 mer 57% conserved"
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/note="forced join made in TA repeat; gap sized to be
600-700bp by restriction digest"
17099..17406
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/note="Single clone region; region covered by PAC PCRs"
17642..17732
/note="MIR repeat: matches 64..154 of consensus"
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/note="59 copies 2 mer aa 59% conserved"
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repeat_region 23088..23138
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repeat_region 23971..24442
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25113..25755
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32999..33066
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Db 100940 TAGGTCATTGACACACATTGATTTTACCATTATGACAGACGATGCTTT-CAGTT 100882
QY 4854 gttatgcatcgtgtagcttcttcacgaagtgtctgtagttcttctctagaagtgct 4913
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QY 5034 actgattgttacaatcaattctgcacatcgaa--ctgctgaattcttctcagttct 5091
Db 100706 ACTGATTGTGTCATTAATTTTGCATCCGAAACTCTGCGAATCTTTTATCATTTCT 100647
QY 5092 gggagcttcttgaggagagctttagaggttctcaggttaaacagctctatcacgaac 5151
Db 100646 AGGAGCTTTTGGAAAAGTCTTAGGCTTTCTTAGGTAATAATCATATCATGACAAAC 100587
QY 5152 aacaagaattgactctctcttcttcttcttcttcttcttcttcttcttcttctg 5211
Db 100586 AGCAACAGTTGACTTCTCTTACTGATTTGAGTCCCTTATTTCTTATCTTGCTG 100527
QY 5212 attctcggtagtaggacttccaactcttcttgaagaagtgtagaagtagggacctt 5271
Db 100526 ATAGCTCTGGCTAGGACTTCCAGTACTATTAAGAGGGGTGAGATGGGAATCTT 100467
QY 5272 tgcctaccagcttctcagaaggagcttctcaacttccatctcatatctg 5331
Db 100466 TGCTGTTCCTCACTTCCACAGGGAATGCTTTCCACATTTTCCCATTCACAAATTAATG 100407
QY 5332 gctgtgagttgtcatalagatgcttattacattggaagtagt 5375
Db 100406 GCTTTGTTGTCATGATGACTTTAGTCATGAGTATGT 100363

RESULT 3
CONSOLID 3
LOCUS 3
DEFINITION 166182 bp DNA HTG 27-NOV-1999
PROGRESS *** in ordered pieces.
ACCESSION AL133241
VERSION AL133241.1 GI:6478098
KEYWORDS HTG; HTGS_PHASE2.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166182)
REFERENCE 1
AUTHORS Direct Submission
TITLE Submitted (26-NOV-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continue. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage, etc.
Contig order : 10 6 3 4 8 9 7, 1000 N's separate segments Contig 10
: length 72699 bp
Contig 6 : length 11379 bp
Contig 3 : length 1715 bp
Contig 4 : length 1913 bp
```

```
Contig 8 : length 12095 bp
Contig 9 : length 54546 bp
Contig 7 : length 7987 bp.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
source
1.166182
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/clone_lib="Caltech-D"
/clone="C-2560C21"
7545..75752
/standard_name="R36079 (RH53786 STS42901)"
/note="matching EMBL:R96079; dbESTs:STS42901; Identifiled
using the e-PCR software (G. Schuler)"
BASE COUNT 48652 a 28853 c 29318 g 53357 t 6002 others
ORIGIN
Query Match 4.6%; Score 883.6; DB 33; Length 166182;
Best Local Similarity 79.4%; Pred. No. 3.9e-150;
Matches 1285; Conservative 0; Mismatches 204; Indels 129; Gaps 15;
QY 3850 gaatgattgtgaagaattctctcactctgtggtgtgtctgttaactctgtcactgtt 3909
Db 48032 GTATGATGTTGTAAGATTTTCTCCACTCTGTGGGTGCTGTCTGTTACTCTGCGACTGTT 48091
QY 3910 ccttttcgacacaaaagctctttagtaagtcacagatattactctgtttgtgtg 3969
Db 48092 CCTTTGCCATGCAAAAGCTCTTTA-----CCAGCTATGATCTTTGCTTTATTG 48142
QY 3970 catttcttgggtctgtgtcagaagctcttcgctgaagctaaagtcataagaaggttt 4029
Db 48143 CATATGTTTGGGACTTGTGTATGAATCCTTGCTTAGGCCAAGCTGTAAGAGGCTTTT 48202
QY 4030 tccaatgctctctcagaattttatagttcagaagctttagattgaagctctgactca 4089
Db 48203 TCTGATGTTATCTCTGATGAAATTTTATAGTT----TCTTAGATTTTAACTCAATATCCA 48257
QY 4090 tcttgaagattttgttataagtgtagagtagagtagcagttcattctctcactatgt 4149
Db 48258 TGTGATTTGATTTTGTGTAGGTGAGATGAGATCCAGTTATTTCTTTACATGT 48317
QY 4150 ggttaagcaattatcccaagcagctgttgaagtaggtgtccttcccaactgaagt 4209
Db 48318 GGTACCCCAATTATCTACACCATTTCTTGAAAGAGGTGCTTTCCACATTTATGTT 48377
QY 4210 tttgttctgttcaatgtagtaggtgtgaagtagttggtttattcttgggtcttc 4269
Db 48378 TTTGTTTGC-TTGTGTAATCATGATGAGC--TAAGTATTTGGGTATTTCCGTGTTTGC 48434
QY 4270 tatttgttccttgttctcatgtgacctattttataagagtagccagctgtttagag 4329
Db 48435 TATTTGTTGCATTTGGCCGTGTGCTTATTTTATCCAGTACATGATGATGTTGTTGAT 48494
QY 4330 tgtgacctataagtagtttgaatcagaatgtagtctcagactt-----4380
Db 48495 TGTTGGCTTATAGTATAGTTTCAATCAGTAGTGTGATGCCCTCCAGGTTTGTCTTTT 48554
QY 4422 tttttctgctctggaacatgtagtggtaatttg-atgggaatctgctgaatttg 4480
Db 48615 TTTTTCCTAATTTGGGAAGAAATGATGTTTGAATGGGATTTGGGTGAATTTG 48674
QY 4481 taataacttcttgagcagta-----taatactttc 4510
Db 48675 TAGATTGCTTTGGACATAGTCATTTCTTTGTTGTTTATTTTATTTGTTGTTGCT 48734
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[illegible]

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
RESULT 4 HSDJ689C5/C	HSDJ689C5, 153781 bp Homo sapiens chromosome 20 clone RP4-669C5, *** SEQUENCING IN PROGRESS ***. In unordered pieces.	U118503	U118503.5	GI:6272168	HTG; HTGS_PHASE1. human.	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

REFERENCE
AUTHORS
TITLE
JOURNAL

Eutheria; Primates: Catarrhini; Homnidae; Homo.
1 (bases 1 to 153781)
Smith, M.
Direct Submission
Submitted (30-NOV-1999) Sanger Centre, Hinxton, Cambridgeshire,

COMMENT On Nov 5, 1999 this sequence replaced gi:6249397.

important, that sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known: 800 n's separate segments. Contig_ID: 0005 Length: 4731bp

Contig_ID: 00425 Length: 6774bp
Contig_ID: 00588 Length: 8407bp
Contig_ID: 00611 Length: 1793bp
Contig_ID: 01464 Length: 6794bp
Contig_ID: 01540 Length: 36855bp
Contig_ID: 01547 Length: 1133bp
Contig_ID: 01811 Length: 16724bp
Contig_ID: 01841 Length: 3357bp
Contig_ID: 01945 Length: 28773bp
Contig_ID: 02026 Length: 2291bp
Contig_ID: 02112 Length: 20276bp.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES	source	Location/Qualifiers
	1.	153781
		/organism="Homo sapiens"
		/dp_xref="taxon:9606"
		/chromosome="20"
		/clone="RP4-689C5"
		/clone_1b="RPCT-4"
BASE COUNT	42510	a 28132 c 27954 g 45585 t 9600 others
ORIGIN		

Query Match	4.5%	Score	868.6	DB	33	Length	153781
Best Local Similarity	77.9%	Pred. No.	2e-1477				
Matches 1287, Conservative	0	Mismatches	169	Indels	197	Gaps	12

[illegible]

Q7 3910 cctttgcacacaaagctcttagt---ttagtcacagctattatctctggtttt.3965

Db 98601 CCTTTGCCATSCAAAGCTCTTAGTATATATTAGTCCGACTATTATCTTGTGTTTT 98542

Db 98541 ATTGCAATTGCTTTGGGTTCTTGTCATGAATCCCTTGCCATAAGCTAATGCTAGAGA 98482

QY 4025 gttttcccaatgttctctttagaatttttttagtttcgaagtcctcagaatttaagtccttg 4084

QY 4085 atctatcttgagttgattttgtgtatagaagtcgagagatcgagatccagtttcaattctccta 4144

4145 catatgactagccaattatccccagacccaattttttaataagcattatccttcccccactta 4204
 Db 98421 atccaccttgagttgatttttttgataaaggtagagagatgacacatccagttccattcmttta 98362

Db 98361 CAAGTGGCTAGCCCAATTATCCCGAGCACAAATTGTGTTGAAAAAGGGTGTCCTTCCCCCACTTT 98302

4203	atgctctctgcttgcacatgcatcagcgcgcaagcctctctgggcttccatctctctctctggg	4204
98301	atgctctctgcttgcacatgcatcagcgcgcaagcctctctgggcttccatctctctctctggg	98242

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QY 4265 ttctctatcttctccttctgctcgtatgtctcctatcttctatcaagctacccagctcgtcttg 4324
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Db 98241 TTCTCTATTCGCTCCATGCTGATGTGCGCCATTTTATACCAATACCAATGCGTTTTC 98182
QY 4325 ataccagctgacctatgtatgtgttgaatcaggtaatgtatgtatcagatcttctcagat 4380
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98181 GTGACTATGCGCTTATGATGTGTAATAACAGTAGTGATGTGTCACAGATTTGCTTC 98122
QY 4380 -----gtatcaggctctcttcttctgctcctatcaatcaatctttagg 4417
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 98121 TTTTCTTAGTCTTACTTTGGCTATGCGAGCTCATTTTGGTCCATATGAAATTTAGA 98062
QY 4418 atcgcttcttctcagctcgtcgtgaaactcgtatgtatcttcatggaatctcgctgaat 4477
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Db 98061 ATT-TTTTCTTATTTCTGTAAGAAATTAACAGTAGTGATTTGATGGGATTCATGTAAT 98003
QY 4478 ttctagatcttcttctgacatcatcatcttctcag----- 4513
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Db 98002 TTGACTATGCTTTTGGAGATGCTATTTTACAAATTAATTCACCATCCACGAG 97943
QY 4513 ----- 4513
Db 97942 CATTGGATGTTTTTCATTTGTTGCTAGCTTGAATTTCTTTCTTTCTTTCTTCT 97883
QY 4513 -tttttttttctctcgaagacagatctcgtctcgtc-gccaggctgattgcaatgagcg 4570
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 97882 TCTTTTCTTTTCTTTTGGAGACAGAGTCTTCTGCTGACCCAGCTGAGAGTGGAG 97823
QY 4571 tgcctct-tgcctgacctcga--cctctgcctcgtggttcaagaatctcctgcctcag 4627
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Db 97822 CAATCTAGGCTCAGTCAACTCTCTCATCTCTGGGTTCAAGCAATTTCTTCTGCTCAG 97763
QY 4628 cctcccaagctcgtgagctacacagc--gcacatcacgcccaagctaatcttcttctt 4684
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 4685 tagtagagacgagggttccacacatgttagcagagctggtctcgtatctctgaacctgtagc 4744
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Db 97702 TAGTAGAGTGGGGGTTTACCATGTTGTGATGAGCTGGTGTAAACCTCTTAACTCGTAT 97643
QY 4745 cctccgcgcctcgcgcctcccaagctacagctacagcgttagcagcgcgcgcgcgcct 4804
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Db 97642 CCACCCGCGCTGCGCTCTCAAGTGTGGGATTACAGCATGAGCCACCAAGCC----- 97588
QY 4805 tcgcaatataatcttctcctacccgttagacatgagatgtcttctcttcttctatgcata 4864
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Db 97588 -----CAAAAGT 97582
QY 4865 ctgtgatctcttccagcagctgtctgtagcttctcctgttagaagctgttcaacctccttg 4924
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Db 97581 CTTTGTATTTCTTTCACAGAGTGTGTTGATTTCTTGTAGAGCTCTTTGACCTCTTGG 97522
QY 4925 ttggatatactcctaagatcttcttcttcttcttcttctgagcgtatcttagaagggttga 4984
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Db 97521 TTAGGCAATTTCCGCGAT-----TTTTTTTTTCAGCTAATTAATAAGGGGTTGA 97472
QY 4985 gtctcttatttattctcagctgtgtctgtgtgtgtatagaaagacactagcttctgtc 5044
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Db 97471 GTTCTTATTTGATTCCTCCACTTGATCATCTGTGTGTGTGAAGAAGACTACTGATTTG 97412
QY 5045 taacataatttgcatactggaac--tgcctgaattcttcttctacagctctggagagcttct 5102
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Db 97411 TACATTAATCTTGTATGTGAATACTTGTGTAATCTTTATATCAGTCTTGAAGACTTTCT 97352
QY 5103 gggaggagcttcttggaggttctcgtgtaaacagctcttctacagcaacaacagcttct 5162
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Db 97351 GGAAGAGATCTTGAAGGTTTCAAGTAACATCTTATTCATACACCAACAGTGTGCACTTT 97292
QY 5163 gactctctcttactgatttggatgctccttacttcttctctctgtctgtatcttctcggg 5222
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 97291 GACTTCTCTTTTACCGAATTTGGATGCCCTTATTTCTTCTGCTGTGATGTGCTCCCTC 97232
```

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QY 5223 taggactccaactcttcttgaagagagtgtaagatggtgcatcttcttctatctc 5282
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Db 97231 TAGGACTCTCCAGTCAATGTTGAAGAGAGTGTGAGAGGCGCATCTTGTCTTCTCC 97172
QY 5283 agttcgaaggagacgcttctcacttctccatctcatattatgttgcgtcgtggtt 5342
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Db 97171 AGTTCACAGGGAATGCTTCAACTTTCCCATTCAGATATACATTTGTTGTGGGTTT 97112
QY 5343 gtcatagtgcttcttattacattgagtgatgt 5375
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 97111 GTCATAGATGCTTTTATTTACATGAAGGTATGT 97079

RESULT 5
LOCUS HSL124H12 30110 bp DNA PRI 23-NOV-1999
DEFINITION Human DNA sequence from cosmid L124h12, Huntington's Disease
ACCESSION 249918.1 GI:887461
VERSION 4p16.3.
KEYWORDS 4p16.3.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 30110)
AUTHORS Dodsworth,S.
TITLE Direct Submision
JOURNAL Submitted (26-JUN-1995) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1RO, England. E-mail: goes@sanger.ac.uk
COMMENT IMPORTANT: This sequence is not the entire insert of clone
L124h12. It may be shorter because we only sequence overlapping
between neighbouring submissions.
The true left end of clone L124h12 is at 1 in this sequence. The
true right end of clone Hw2 is at 18185.
The true left end of clone L108f12 is at 30011.
The start of this sequence (1..100) overlaps with the end of
sequence 249235 ( L108f12 ).
The end of this sequence (30011..30110) overlaps with the start of
sequence 249235 ( L108f12 ).
L124h12 is from cosmid library LA04NC01 constructed at the Human
Genome Center, Los Alamos National Laboratory, NM 87545 under the
auspices of the U.S. Department of Energy. The library was
constructed using flow-sorted human chromosome 4 from a
Hamster-Human hybrid cell line ( UV20HL21-27 ) containing human
chromosomes 4, 8 and 21.
VECTOR: sCos1
L124h12 is contained in a clone contig spanning
2Mb which is described in Baxendale et al, Nature Genetics 4 ( 1993
) 181-186. See also Myers et al, Cytogenet Cell Genet. 66 ( 1994
) 218-230.
FEATURES
source 1..30110
location/Qualifiers
1..30110
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/map="4p16.3"
/clone_1fb="LA04NC01"
/cell_line="UV20HL21-27"
/clone="LA04NC01-124H12"
1..59
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/partial
/note="Alu repeat: matches 62. .1 of consensus"
242..532
/note="Alu repeat: matches 308. .1 of consensus"
1440..1716
/note="Alu repeat: matches 1. .308 of consensus"
2368..2451
/partial
/note="Alu repeat: matches 59. .150 of consensus"
2609..2779
/note="MITE element fragment"
```



```
repeat_region 4077..4354 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 4512..4766 /note="L1 element fragment"  
repeat_region 4984..5045 /note="Alu repeat: matches 308. .37 of consensus"  
repeat_region 5115..5406 /note="MER7 element fragment"  
repeat_region 5409..5512 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 5501..5548 /note="MER29 element fragment"  
repeat_region 5673..5890 /note="MER17 element fragment"  
repeat_region 6124..6496 /note="MER29 element fragment"  
repeat_region 6503..6835 /note="MER17 element fragment"  
repeat_region 7568..7747 /note="MER18 element fragment"  
repeat_region 7754..7802 /note="Alu repeat: matches 277. .69 of consensus"  
repeat_region 7977..8201 /note="Alu repeat: matches 48. .1 of consensus"  
repeat_region 8202..8491 /note="MER4A2 element fragment"  
repeat_region 8495..8753 /note="Alu repeat: matches 1. .308 of consensus"  
repeat_region 8768..8930 /note="MER4A2 element fragment"  
repeat_region 11621..11925 /note="Alu repeat: matches 129. .308 of consensus"  
repeat_region 11929..12012 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 12013..12054 /note="Alu repeat: matches 142. .60 of consensus"  
repeat_region 15142..15215 /note="Alu repeat: matches 205. .164 of consensus"  
repeat_region 15540..15632 /note="37 copies of 2mer 81 & conserved"  
repeat_region 15842..16121 /note="L1 element fragment"  
repeat_region 17390..17691 /note="Alu repeat: matches 296. .1 of consensus"  
repeat_region 18254..18336 /note="Alu repeat: matches 1. .308 of consensus"  
repeat_region 18370..18581 /note="Alu repeat: matches 308. .224 of consensus"  
repeat_region 18818..19106 /note="Alu repeat: matches 226. .1 of consensus"  
repeat_region 19149..19434 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 19483..19775 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 20111..20402 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 20584..20872 /note="Alu repeat: matches 1. .308 of consensus"  
repeat_region 21074..21363 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 22237..22573 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 22720..24165 /note="L1 element fragment"  
repeat_region 24188..24479 /note="L1 element fragment"  
repeat_region 24480..25929 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 25954..26244 /note="L1 element fragment"  
repeat_region 26273..26374 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 26484..26773 /note="L1 element fragment"  
repeat_region 26777..27337 /note="Alu repeat: matches 308. .1 of consensus"  
repeat_region 27340..27616 /note="L1 element fragment"  
repeat_region 27628..27913 /note="Alu repeat: matches 308. .16 of consensus"  
repeat_region 28030..28740 /note="L1 element fragment"
```

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GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 28, 2000, 10:38:02 ; Search time 12284.3 Seconds
(without alignments)
6147.117 Million cell updates/sec

Title: US-09-339-352-7_COPY_1_20000
Perfect score: 20000
Sequence: 1 gatcattcgttctcaggcc.....gaacttagattctcttgya 20000

Scoring table: IDENTITY_NUC

Searched: 4538634 seqs, 1887831982 residues

Database: EST:*

Word size: 0

Number of hits that pass the threshold: 9077268

1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
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50: gb_est31:*
51: gb_est32:*
52: em_est20:*
53: em_est21:*
54: em_est22:*
55: em_est23:*
56: em_est24:*
57: em_est25:*
58: em_est26:*
59: gb_est33:*
60: gb_est34:*
61: gb_est35:*
62: gb_est36:*
63: gb_est37:*
64: gb_est38:*
65: em_est27:*
66: em_est28:*
67: em_est29:*
68: em_est30:*
69: gb_est39:*
70: gb_est40:*
71: gb_est41:*
72: gb_est42:*
73: gb_est43:*
74: gb_est44:*
75: em_est31:*
76: em_est32:*
77: em_est33:*
78: em_est34:*
79: gb_gss1:*
80: gb_gss2:*
81: gb_gss3:*
82: gb_gss4:*
83: em_gss1:*
84: em_gss2:*
85: em_gss3:*
86: em_gss4:*
87: gb_gss5:*
88: gb_gss6:*
89: gb_gss7:*
90: gb_gss8:*
91: gb_gss9:*
92: em_gss5:*
93: em_gss6:*
94: em_gss7:*
95: em_gss8:*
96: em_gss9:*
97: em_gss10:*
98: em_gss11:*
99: gb_gss10:*
100: gb_gss11:*
101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	472.4	2.4	493	81	B36003
2	443.8	2.2	842	89	A0897632
3	420.4	2.1	590	82	A0706541
4	410.8	2.1	501	63	A1950087
5	405.6	2.0	524	49	AL049113
6	391.8	2.0	457	25	N70208
7	391.2	2.0	646	104	AC545781

```

c 8 389 1.9 405 90 B99738
9 386.8 1.9 422 30 AA251874
10 380.8 1.9 473 31 AA283144
c 11 373.8 1.9 538 100 AO277241
c 12 371.2 1.9 579 100 AO316362
c 13 357 1.8 2971 80 AF101960
c 14 355.8 1.8 866 87 AO752136
c 15 324.4 1.6 2971 80 AF101960
c 16 322.8 1.6 666 24 N36809
c 17 319.4 1.6 695 43 A1174916
c 18 313.8 1.6 599 90 AO058824
c 19 308.4 1.5 334 34 AA488964
c 20 306.6 1.5 547 82 AO694304
c 21 296.4 1.5 559 61 A1819225
c 22 288.2 1.4 582 102 AO417202
c 23 287.2 1.4 500 61 A1821380
c 24 285.4 1.4 688 81 B69266
c 25 284.4 1.4 731 103 AO474778
c 26 283.6 1.4 727 103 AO484818
c 27 283 1.4 428 91 AO129730
c 28 282.8 1.4 689 79 AO019547
c 29 282.4 1.4 702 102 AO395067
c 30 282.2 1.4 520 81 B60352
c 31 282 1.4 469 82 AO692948
c 32 282 1.4 555 105 AO629757
c 33 281.6 1.4 490 81 B39755
c 34 280.4 1.4 812 81 B05781
c 35 279.6 1.4 732 90 B94490
c 36 279.4 1.4 730 89 AO898190
c 37 279.2 1.4 516 90 AO003835
c 38 278.4 1.4 737 91 AO116454
c 39 278.2 1.4 463 42 A1089421
c 40 277.8 1.4 306 25 M46026
c 41 277.8 1.4 621 100 AO269192
c 42 276.8 1.4 403 35 AA594479
c 43 276.6 1.4 509 102 AO381842
c 44 275.6 1.4 474 81 B39296
c 45 275.2 1.4 827 82 AO741201
```

ALIGNMENTS

```

RESULT 1
LOCUS B36003 493 bp DNA GSS 17-OCT-1997
DEFINITION HS-1031-A2-H02-MR-ab1 CIT Human Genomic Sperm Library C Homo
sapiens genomic clone Plate-CT 811 Col-4 Row-O, genomic survey
sequence.
```

```

ACCESSION B36003
VERSION B36003.1 GI:2535372
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
```

```

REFERENCE 1 (bases 1 to 493)
AUTHORS Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,
Traioccoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
TITLE Construction of a Characterized Clone Resource for Genomic
Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
Tagged Connectors
JOURNAL Unpublished (1997)
COMMENT Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackrone@u.washington.edu
Sequence Tagged Connector
Plate: CT 811 row: O column: 4
Class: BAC ends
High quality sequence stop: 493.
```

```

FEATURES
source Location/Qualifiers
1..493
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-CT 811 Col-4 Row-O"
/clone_11b="CIT Human Genomic Sperm Library C"
/sex="M"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT 119 a 124 c 108 g 141 t 1 others
ORIGIN
```

```

Query Match 2.4%; Score 472.4; DB 81; Length 493;
Best Local Similarity 99.6%; Pred. No. 7.9e-44;
Matches 473; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 786 atgtgacttcttgagacatttgaccagatgtcctctgtttaaggacaaattagaatt 845
|||||
DB 19 atgtgacttcttgagacatttgaccagatgtcctctgtttaaggacaaattagaatt 78
|||||
QY 846 ctcaacttgcacaaacacacagtagaactaagctagtcacatcctcttttttttt 905
|||||
DB 79 ctcaacttgcacaaacacacagtagaactaagctagtcacatcctcttttttttt 138
|||||
QY 906 gtagatgagcttcaactctgtgttcgcaagctgtagtgaatgtagtctgcgtcacty 965
|||||
DB 139 gtagatgagcttcaactctgtgttcgcaagctgtagtgaatgtagtctgcgtcacty 198
|||||
QY 966 caactctgcctctctgtgttcaagagattctctgcctcagcctcttgatgtagtggat 1025
|||||
DB 199 caactctgcctctctgtgttcaagagattctctgcctcagcctcttgatgtagtggat 258
|||||
QY 1026 taaaggacacacacacacacacacacacacacacacacacacacacacacacac 1085
|||||
DB 259 taaaggacacacacacacacacacacacacacacacacacacacacacacacac 318
|||||
QY 1086 acatgtttgacacagctgtgtctgcaactctgcaactcagtgtagtgcacacgtcgcct 1145
|||||
DB 319 acatgtttgacacagctgtgtctgcaactctgcaactcagtgtagtgcacacgtcgcct 378
|||||
QY 1146 ccccaagtcgtggtgattacaggtgtgagctgacgtcctcttattagtagacacagcta 1205
|||||
DB 379 ccccaagtcgtggtgattacaggtgtgagctgacgtcctcttattagtagtagacacagcta 438
|||||
QY 1206 acgaaacataaatgagcactcttttgaagactgagagccttgagatctccctagac 1260
|||||
DB 439 acgaaacataaatgagcactcttttgaagactgagagccttgagatctccctagac 493
|||||
```

```

RESULT 2
LOCUS AO897632/c 842 bp DNA GSS 10-NOV-1999
DEFINITION HS_3135-AL_A10-T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate-3135 Col-19 Row-A, genomic survey
sequence.
ACCESSION AO897632
VERSION AO897632
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 842)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,K.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
```

University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 3135 row: A column: 19

Seq primer: T7
Class: BAC ends
High quality sequence stop: 842.

FEATURES

source

1. 842
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-3135 Col-19 Row-A"
/clone_11b="CIR Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 261 a 155 c 98 g 326 t 2 others
ORIGIN

Query Match 2.2%; Score 443.8; DB 89; Length 842;

Best Local Similarity 84.0%; Pred. No. 8.9e-41;

Matches 624; Conservative 0; Mismatches 94; Indels 25; Gaps 10;

OY 18886 gcaaaattatgtaaaagagtgatattgtaaaattctgtcttgaataaataact-18945
DB 733 GGAGATTTATGTAAANAGATCTTAAGTGAATTTCTGCTTAAGTAACTTANCTG 673
OY 18945 gtgtttaagaagaataattgtaataagtcagaagtgtgacatgtcaagaatta 19004
DB 672 GTTGTTAAGAAAGGAGTGT-----TACATCAGAAAGTTAAGCATGCAAG-ATTG 619
OY 19005 tctgtgaagtcataagaacagctgtatacaaaaattatgcaaaaatattgtataat 19064
DB 618 TGTGGAAGATCAT-GAANAATTATTAANAAGATTTATGCAAGAAATGTTGACAAAT 560
OY 19065 tgaagtaataagccctcctgtgt-----actatgagaagaacagtttattgtgcaggtg 19119
DB 559 TGAAGTAAATTAAGCCCTCTCGATGAATTAAGAACTATTGAAGACAGCTTTATGTCAAGTG 500
OY 19120 cataagaaagtaaaataactttgtgttaaaagattagaagagcacaagaattgtga 19179
DB 499 TGTAAAGAAAGTAAATATATCTTAGGTAAAGATTATAGGAGCAATGCGA 440
OY 19180 ttttaaccataaaaggttaaaaaaattattgtttgaaagtttaagcaagtttaa 19239
DB 439 CTTTATACCTACATTAAAGATTAAAAA-----AGTTTGAAGGTTTAAGCAAGTTTCA 384
OY 19240 aatgttaattgtaaaaaaattctgtgtgttaactaattagctaaagataaaagttat 19299
DB 383 AACGTTAATGT-AAAAGAAATTCGTGTGTAAACATATGGCTAAAGTTAAAGGGGTAT 325
OY 19300 cat-----ccagttttctgtgttaactgtgacattaaagtaaaatgcagagtttctt 19354
DB 334 CACCCAGCCCACTTTTCTGTGACGACATTAAATAAAGCAACAAAGCCTTTTCTT 265
OY 19355 gaagaccacacgtctctttaaacaanaattataaaggttaaaagtcgttaaaaa-c 19413
DB 264 AAAGCACTTAACCTGCTCTTTAATAAATTAATAAGGTTAAAGAGCTTATAAATTC 205
OY 19414 ttacctatgtgtcaaacatgtaaaattgtgataataatgtctatgaggtttttaaaatt 19473
DB 204 TTAAGTTATGTCAGACAT-TAAATTTGATTAATATGCTCAAGGTTTATTAAATTT 146
OY 19474 aagtttaacattataaacacactaataataaaggttaaaatttgctctatgtgtataaaaa 19533
DB 145 GAGTTTAACTAATTAATTAATCACTAATATATAAGTTAAATTTAGTTCATGTGATTAATA 86
OY 19534 tcatacaagaagatattataataataaaatgtgttttagcttcttcttgcataaaacta 19593

DB 85 TCATACAGCAACACTGTAATATATAATGCTGTTGCTTGTGTCTACAAACA 26
OY 19594 ataaaaataggtcctaaggaat 19616
DB 25 ATTAATAACAGCTGTTTACAGTAA 3

RESULT 3

AOJ06541/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

99380589

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

or from Resear h Genetics (info@resgen.com). BAC end Web Server:

<http://www.htsc.washington.edu>

Plate: 1110 row: L column: 23

Seq primer: T7

Class: BAC ends

High quality sequence stop: 590.

Location/Qualifiers

1. 590

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Plate-1110 Col-23 Row-L"

/clone_11b="RPCI-11 Human Male BAC Library"

/sex="male"

/note="Vector: pBACe3.6; Genomic sequence of BAC ends"

BASE COUNT 143 a 135 c 122 g 181 t 9 others

ORIGIN

Query Match 2.1%; Score 420.4; DB 82; Length 590;

Best Local Similarity 90.9%; Pred. No. 4e-38;

Matches 500; Conservative 0; Mismatches 42; Indels 8; Gaps 5;

OY 16060 acacattatctctccctctctctgtgagagccctctgagggcagagagacatta 16119
DB 579 ACACATATCTCTCTCTCTCTGTGTGAGAGCTCC-TGAGCAAGAGAGAGTC-TTA 522
OY 16120 ttgatattcaagggcttggcaattgtgacacatgtcccaaatctcatgttaattc 16179
DB 521 TTGATATTCAGGG-TTGGCACTTGT---ACACATGTCACCAATTTATATGTAAATTC 466
OY 16180 ttgaccttagggcctcaaatgtgtacattttgaaagaagagtcgtgtgcagatacat 16239
DB 465 TTAGCCTTAGGGCCTCAAGTGTC-CATTATTTGAAGAAGAGTCGTTGCGATACAAAT 408

QY	16240	tagtaagaatgagatcatgctctaggttaggttaggcctctaactcaataaactgtgccc	16239
Db	407	TAGTAAATGATGATCATGCTCTGAGCTAGAGTGAGGCTCTTAATCCATTAACCTGATGCC	348
QY	16300	ttataaaaaaggaaatttggacacacaacacacacagggaggaatgccaatgtgacatgaa	16359
Db	347	TTATAAAAAGGAGAAATTTGGACACACAAACACACANAGGAGAAATGCCATGTGACATGAA	288
QY	16360	ggcaagaatttaggtgtgagacgctctgaacgccaactcttggaaacacgaagaatggcagcaa	16419
Db	287	GGCAAGATTTAAGGTGTGACGCTTCTTCAAGGCCATCTTTGGAAACACAAAGATGGCCAGCAA	228
QY	16420	ccaccagaagcttagcaggttggcgaatgaacagatcttcctcatgtgtccagsgaaanaa	16479
Db	227	CCACACAGAGCTAGCAGGTGGGCGACAGAAACAATTTCTTCATGATGTCACAGAGAAANA	168
QY	16480	gatgccttgatctcagatctcctaccccctggagaacatgagaanaattctgtgtgaagcc	16539
Db	167	GATGCTTGATCTCAGACTCTCTACCCGCGAGACATATGAGACAAATNTCTGTGTGAAGCC	108
QY	16540	atccctctgtagtaacttttttcaagaagccccgcgcttagtgaataacgaacttagtagtc	16599
Db	107	ATCCATTGTGTACTTNTNTACAGAGGCCGCGGCTAGTGATACAGCACTTAGTAGTTC	48
QY	16600	ctgaacatag 16609	
Db	47	NNGAACATAG 38	
RESULT	4		
LOCUS	A1950087		
DEFINITION	wq05c02.x1 NC1_CGAP_Ki012 Homo sapiens CDNA clone IMAGE:2470370 3'		
ACCESSION	A1950087		
VERSION	A1950087.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
AUTHORS	Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 501)		
JOURNAL	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Unpublished (1997)		
	On Feb 17, 1998 this sequence version replaced gi:2889741.		

FEATURES
source

```

seq primer -40UP from Gibco
High quality sequence step: 388.
Location/Qualifiers
1. 501
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2470370"
/clone_1bp="NCI_CGAP_K1d12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH108"
/note="Organ: kidney; Vector: p7T73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_K1d5 was
prepared, and ss circles were made in vitro. Following HAP

```

BASE COUNT 164 a 86 c 88 g 163 t
ORIGIN

Query Match	Identity	Score	DB	Length
Best Local Similarity	93.1%	Pred. No. 5e-37		
Matches	430	Conservative	0	Mismatches 32; Indels 0; Gaps
OY	19439	ttggaataatgctatgtagggtttattataaattgaattcaacttaatacactaa	19498	
Db	24	TTGGATAAATATTTTACAGGTTTTATTAATTAAGTTTACATATATAACACTAA	83	
OY	19499	tataaggtaaatattagcttctcggataaataatcacagaagtataataat	19558	
Db	84	TATAAGGTAATTTACTTATCTCGTATATAAGTCATACGGAAAGCTTGTAAATAT	143	
OY	19559	aaatggtgttagcttcttccttggtctaaataataaataaggtccctaaggaaaca	19618	
Db	144	AAAAAGGGTTAGCTTCTTTTGTCTAAAACTATATAAATTTGGTGAAGGAGCA	203	
OY	19619	ttcattttactagagatcatagaagttaaagacttaaaacaacttggcaattaagac	19678	
Db	204	TTCAATTACTAGAGATCATATAAGTTAAAGTTAAACACTTGGCAATTAAGAC	263	
OY	19679	agcataccaagatgcaaatgcccgtgtgaaatgatatcaaatcttcacatctgcaattaa	19738	
Db	264	AGCATACCAAGATGCAAAATGCTCGGTGTAAGATCAAAATTTCCATCTGCAGGTTAA	323	
OY	19739	caaaagcagttcttatgctgtgcacatgagcagagcagaagcccacattgtcccttcc	19798	
Db	324	CAAAAGCAATTAGCATGCTTGTGCAATGGCAGGCCAAGAACCTTGATGTGCCCTTTC	383	
OY	19799	actaaagtgtctcccaatgccacagcgctgggtctgacatgtagctctttccagagatc	19858	
Db	384	ACTAAGTGTCTCCCTCAGTCGGCCAGGAGATGGGTGATGTCATGTCCTTTCCAGATTCC	443	
OY	19859	tacagctcgagataatagatctgccaactctctctat	19900	
Db	444	TATACCTGGAGTATTAAGTCATGCCAAGCTTCTCTGCTAT	485	

RESULT	5								
LOCUS	AL049113								
DEFINITION	AL049113	524 bp	mRNA	EST	29-SEP-1999				
ACCESSION	DKEZ2434D1519	rl 434	(synonym: htes3)	Homo sapiens	cDNA clone				
VERSION	DKEZ2434D1519		mRNA sequence.						
KEYWORDS	AL049113								
SOURCE	AL049113.1	GI:4728423							
ORGANISM	EST.								
REFERENCE	human.								
AUTHORS	Homo sapiens								
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;								
	Eutheria; Primates; Catarrhini; Homidae; Homo.								
	1 (bases 1 to 524)								
	Ottenwaelder, B., Obermayer, B., Mewes, H.W., Gassenhuber, J. and								
	Wiemann, S.								
TITLE	EST (Ottenwaelder, et al.)								
JOURNAL	Unpublished (1995)								
COMMENT	On Jun 5, 1998 this sequence version replaced gi:3189292.								

Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ): Email: s.wiemann@dkfz-heidelberg.de;
sequenced by MedGenomix within the CDNA sequencing consortium of
the German Genome Project.

No si sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Source

Location/Qualifiers
1..524

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZP434D1519"
/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI"
BASE COUNT 99 a 131 c 153 g 141 t
ORIGIN

Query Match 2.0%; Score 405.6; DB 49; Length 524;
Best Local Similarity 88.7%; Pred. No. 1.8e-36;
Matches 479; Conservative 0; Mismatches 44; Indels 17; Gaps 3;

Qy 17479 actccctcactatcgcgtgctgaagggtttgtctgcggctcactcgtctaacattc 17538
|||||
Db 1 ACTCCCTCACAATCTTGCTGCTGAGGGGCTTTGCTCGGCTGCTCCTGCTACATTC 60
Qy 17539 ttgttccctgcagcggaagcagagtgtataacagatgtgtcagagcagctccttagcg 17598
|||||
Db 61 TTGGTTCCCTGCACGAGGAGCGAGGTGATTAAGGTTGAGGAGCTCCTTAGGCCA 120
Qy 17599 ctttagcctccctgtgaacacccctgctggtggaactccaaccagccagagtgagcg 17658
|||||
Db 121 CTTTAGCCTGCCCTGTGACATCCCTGCGGGGACTCCAAACAGCCAAAGCAAGCGGA 180
Qy 17659 tccctgaagctcctcgtgtgaagcattgccccggctggaacccctgcagagcagtg 17718
|||||
Db 181 TCCTAGAGTGTCTCTGGGTAGGCACTTGCCCTGATGGAGCCCTTGCCAGAGCAGTGT 240
Qy 17719 tggcagggcccccgtggaagataacacagatgtgtgaacacgggaagaaattggcact 17778
|||||
Db 241 TGGCAGGGCCCCGTGAGAGATCAGCAGTGGCTGAACACGAGGAAGAACTGCATTGG 300
Qy 17779 gagtcggacaactaaactgtgtaagactagtcttggaaacttgcacatcattgg 17838
|||||
Db 301 GAGTGTGACATCTAAACTGTGTAAGACTTGTCTTGGAACTTGCCCTCCTCATTGTG 360
Qy 17839 tggagacatgacctatcacccacgctgtccttatacagcac-ttggtttggtttga 17897
|||||
Db 361 TGGAGCATGGCCTCATATCCACGGTGTGCTTATCGGCACATTGGTTGGTTTGA 420
Qy 17898 ctgtgttaactacttgcacaggaactgtcttgggaacttgcacacatccatccactc 17957
|||||
Db 421 CATGTTTGAATTCCTTGCAGGGTGTGCTTGGGAATTTG-----CCTCTAC 469
Qy 17958 atttgaatggaagcagctgcatctgataccacacggtgtcctgttcggcacttgg 18017
|||||
Db 470 ATTGAGCGGAAGCATGGC-----CTGATCACCATGGCGTCTGTACCGGCACTTTGG 524

RESULT 6

N70208 457 bp mRNA EST 14-MAR-1996
LOCUS za55e09.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
DEFINITION IMAGE:296488 3', mRNA sequence.

ACCESSION N70208.1 GI:1226788
VERSION N70208
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 457)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

TITLE
JOURNAL
COMMENT
The Washu-Merck EST Project
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785235.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through INFL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: ml3 -40 forward
High quality sequence stop: 379.

FEATURES

Source

Location/Qualifiers
1..457

/organism="Homo sapiens"
/db_xref="GDB:1241409"
/db_xref="taxon:9606"
/clone="IMAGE:296488"
/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT773D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' AATCGAAGATTAATTAAGATCTTTTATTTTATTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT773 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 157 a 83 c 84 g 132 t 1 others
ORIGIN

Query Match 2.0%; Score 391.8; DB 25; Length 457;
Best Local Similarity 93.7%; Pred. No. 6.5e-35;
Matches 419; Conservative 0; Mismatches 27; Indels 1; Gaps 1;

Qy 19449 atgtctatgaggtttatataaattgaattacaattataacacataataaagta 19508
|||||
Db 1 AATGCTACAGGCTTTATTAATTAAGTTTAACTATTAACACACTTAATTAAGGTA 60
Qy 19509 aaatttaactatcgtgataaataacacagagatattataataaataatggt 19568
|||||
Db 61 AATTTAGCTTATCTGATTAATAAATCATACGAGAGCAATTGTAATTAATAAGCT 120
Qy 19569 ttagtcttccttggtctataaataataaataagttccataaaggaacatcatttac 19628
|||||
Db 121 TAGCTTTCTTTGTCTTAATAAATTAATTAATTAATTAATTAATTAATTAATTA 180
Qy 19629 tagagatcatagaagttaaagaactaaacaaacttggcaattaaagaacgacataca 19688
|||||
Db 181 TAGAGATCATTAAGTTAAAGCTTAACAACTTTGGCAATTAAACAGCATACCA 240
Qy 19689 gatgaatgcctgtttataatgataataattccatcgtacataataaagaagcag 19748
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Db 241 CATGCAATGCTGTGTAATGAATGATCAATTAATTCATCTGAGGTTAAACAAAGCAT 300
Qy 19749 tgttatgtcttgacatgagcagcagagcccatcattgtcccccctccataaagtgg 19808
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Db 301 TAGCATGCTTGTGACATAGCGAGCCAGAGACCTTGATTTGCCCTTCCACTAAGGTGG 360
Qy 19809 tcttcagctc-cacagagcggtggtgcatgtgtagctctttccaggaattcaagcctg 19867
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Qy 19868 gagtaataagtcattccaaactctctc 19894

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Db      421 GAGTAATAAGTCATGCCAAGCTCTCTC 447
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RESULT  7
LOCUS   A0545781      646 bp      DNA
DEFINITION CITBI-E1-2629B18.rf CITBI-E1 Homo sapiens genomic clone 2629B18,
genomic survey sequence.
ACCESSION A0545781
VERSION   A0545781.1  GI:4905024
KEYWORDS  GSS.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
           Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 646)
AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
           Venter,J.C.
TITLE      Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
           Map Building
JOURNAL   Unpublished (1997)
COMMENT    Contact: Shaying Zhao, William Nierman, Mark Adams
           Department of Eukaryotic Genomics
           The Institute for Genomic Research
           9712 Medical Center Dr., Rockville, MD 20850
           Tel: 301 838 0200
           Fax: 301 838 0208
           Email: hbe@ligr.org
           Clones are available from Research Genetics (info@resgen.com). BAC
           end search page:
           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
           Seq primer: M13-21
           Class: BAC ends.
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  source          1..646
                   /organism="Homo sapiens"
                   /db_xref="taxon:9606"
                   /clone="2629B18"
                   /clone_1id="CITBI-E1"
                   /sex="male"
                   /cell_type="sperm"
                   /note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
                   Caltech Human BAC Library D"
BASE COUNT      206 a      126 c      70 g      244 t
ORIGIN
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Best Local Similarity 81.0%; Pred. No. 6.5e-35;
Matches 530; Conservative 0; Mismatches 113; Indels 11; Gaps 6;
QY 18946 ttgtttaagaagaataatttgttaataagtcagaagaagtcagacatgccaagaattat 19005
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QY 19006 ctggaagaagtcataagaacgatgttataaaattatgcaaaaataatgttaattt 19065
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Db      587 CTGTGGAAGTATGATAAAATGTTATTAAGAAATTTATGACAGAAAGTGTCATAATT 528
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QY 19066 gaaagtaaaagcctcctg-agtactatgaagaacagttatgtcgaagtgcataa 19124
|||||
Db      527 AAAAGTAGGCTCTCGCTGTGAAGAACTTTGAAGAAACAGTTTATGTCAGAGTGCTGTA 468
|||||
QY 19125 gaaaagtaaatatacttctgtgtaaaagatcagaagagcacaagaatgtgattttc 19184
|||||
Db      467 GGAAGTAATAATATCTTTGTGAAGAAATTTATGAAGAGCCATAAGATGTGATTTT 408
|||||
QY 19185 accacacataaagggttaaaaaattatgtttgaaagtttaagcaagtttaaatgt 19244
|||||
Db      407 ACCTACATTTAAAGGTTTAA-----ATTGTTTGAAGGTTTAAAGCAAGTTTGAAGCGT 354
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QY 19245 taattgtaaaaaaaatctgtgtgtaaacctaattagctaaagataaaagtatcatcc 19304

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Db      353 TAATTGT-AGAGGAAGTTCTGTGTGAACATATTGGCTAAAGTTAAAGGGATGATCATCC 295
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QY 19305 agttttctgtgaactggacattaagaatgaataaatgcaacagagttttcttgaagcccaa 19364
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Db      294 AGTTTCTGTGAACAGGACATTTTAATTAAGCACAAATGGGTTTTTCTTAAAGCACTAA 225
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QY 19365 cctgctcttaacaaaattataaaggttaaaagagtcgtgaanaacttaccattatgg 19424
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Db      234 CTGTGTTTAAACAAAATATATAGAGGTTAAAGAGTGCCTTAAATAATCTTACCTATG 175
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QY 19425 tcaaacatgaaaaattggataaatatgctcctagaggtttatataaatttaaacat 19484
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Db      174 GTTAGACATTACAAATTGGATAAATATGCTACCAAGATTTTAAATCGAGTTTAACAT 115
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QY 19485 taataacacctaattaaaggttaaaattagcttctgtgtaaaatcatcaaga 19544
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Db      114 TAATAGCACACTAATGAAAAGTGAAAGTTTGAAGATCTGTAT-AAATCCATACAGGA 56
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QY 19545 gtattataataataaatgtgttagctt-cttgctctaaactataa 19597
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RESULT  8
LOCUS   B99738      405 bp      DNA
DEFINITION CIT-HSP-2284G20.rf CIT-HSP Homo sapiens genomic clone 2284G20,
genomic survey sequence.
ACCESSION B99738
VERSION   B99738.1  GI:3026289
KEYWORDS  GSS.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
           Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 405)
AUTHORS   Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K.,
           Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
           Simon,M. and Venter,J.C.
           Use of a random BAC End Sequence Database for Sequence-Ready Map
           Building (1998)
JOURNAL   Unpublished (1998)
COMMENT    Contact: Mark Adams
           Department of Eukaryotic Genomics
           The Institute for Genomic Research
           9712 Medical Center Dr., Rockville, MD 20850, USA
           Tel: 301 838 0200
           Fax: 301 838 0208
           Email: mdadams@ligr.org
           Clones are available from Research Genetics (info@resgen.com). BAC
           end search page:
           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
           Seq primer: M13-21;
           Class: BAC ends.
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                   /clone="2284G20"
                   /clone_1id="CIT-HSP"
                   /sex="male"
                   /cell_type="sperm"
                   /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
                   HindIII"
BASE COUNT      94 a      107 c      72 g      132 t
ORIGIN
Query Match          1.9%; Score 389; DB 90; Length 405;
Best Local Similarity 97.5%; Pred. No. 1.4e-34;
Matches 395; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 9913 catatgacaccactacactcagcttggtgacagagtaagaccctgtctcaaaagaa 9972
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Db 405 CATGATGACACAGACTTACCTGCTGACAGAGTAAGACCTGCTCAAAAGAGT 346
QY 9973 acagaaaaaagaaaaaatttttaaaagtggggcaggaagaatctgtaag 10032
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Db 345 TCAGACACAAACAAATAGAACATTTTAAAGGTGGGCCCAATGAATCTGAATAG 286
QY 10033 gacatcaagacacataaagaatctgtagaagctcagaggaatgtatgcaga 10092
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Db 225 TGTGAGAGTTCAGAAATGGAAGAGGTACTTACAGTCCAGTTCTTGGAGATCCAGCT 166
QY 10153 cacatgaagtcagaagacagatctgttgagatgtcgttaagctgtactgcacaaatgac 10212
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Db 165 CACATTGAGTCAGACAGATCTGTGTGAGATGTGCTTACCTGTACTGACCAATGAC 106
QY 10213 aatgtaagtggtgtctcctgtcttcttatacagccctgcagcctgcagaggaatgtaac 10272
|||||
Db 105 AATGTAGGTGTTCTCTTCTTATATACGGCCCTGCGACAGTGCACAGGGAATGTAAAC 46
QY 10273 gaagggacacaggaacataatgatgataagataaggaagtcaggat 10317
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Db 45 GAAAGGACACAGGACATATGATGAATGAAGATGAAGAGTCCGGAT 1
RESULT 9
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LOCUS zsl0h1.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:584837 5',
DEFINITION mRNA sequence.
ACCESSION AA251874
VERSION AA251874.1 GI:1886854
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (Bases 1 to 422)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On May 18, 1995 this sequence version replaced gi:810999.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
THIS CLONE IS AVAILABLE ROYALTY-FREE THROUGH LNLN; CONTACT THE
IMAGE CONSORTIUM (info@image.llnl.gov) FOR FURTHER INFORMATION.
Insert Length: 889 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 372.
Location/Qualifiers
1. 422
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/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGGCGCCCTCATTTTCTTTTCTTTT-
3']. Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73D vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 146 a 81 c 77 g 118 t
ORIGIN
Query Match 1.9%; Score 386.8; DB 30; Length 422;
Best Local Similarity 94.8%; Pred. No. 2.4e-34;
Matches 400; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 19473 taagtttaacataataacacactaataaaggtaaaatttaagctatctcgtatataaa 19532
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QY 19533 atcatcaagaagattatataataaattggttttagcttcttctgtctataaaact 19592
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Db 61 ATCATACAGAAACATTTTAAATATAATTAATTAATTAATTAATTAATTAATTAATTA 120
QY 19593 aataaaataagtcctaaagaacatcatttactagagatcatagaaatgaagac 19652
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Db 121 AATTAATAATAGTGTCTAAGGAAACATTCATTCTAAGAGACCATACAAAGTTAAAGAC 180
QY 19653 ttaaaacaacttggcgaatataagacagcacaagatgaaatgctgttgaaatg 19712
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Db 181 TTAATAACAACTTTGGCATTTAAGACGCGATACCAAGATGCAAAATGCTGTATTAATAGG 240
QY 19713 atcaaatatcatcctgcacattaaacaaagcagttgttactgtctgtccatctgacag 19772
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Db 241 ATCATATTTTCCATCTGACGCTTAACAAAGCAATGTATTGCTTGTGACGCGGACAG 300
QY 19773 ccagaagccctcatctgtccctccctccactaaagtgtgtcctcagtcacacagcgctggc 19832
|||||
Db 301 CCAAGCGCGTGGATGTGCCCTTCCACTAAGGTGCTCCCAATGCGACGCGGCGTGGC 360
QY 19833 tgcagttagctcttccagagattcacaagcctggagatgaatgaatgaatgaatgaatga 19892
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QY 19893 tc 19894
||
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RESULT 10
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LOCUS zsl14d04.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713095 5',
DEFINITION mRNA sequence.
ACCESSION AA283144
VERSION AA283144.1 GI:1926078
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (Bases 1 to 473)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT On May 8, 1995 this sequence version replaced gi:801207.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
THIS CLONE IS AVAILABLE ROYALTY-FREE THROUGH LNLN; CONTACT THE
IMAGE CONSORTIUM (info@image.llnl.gov) FOR FURTHER INFORMATION.
Insert Length: 999 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 450.
Location/Qualifiers
1. 473
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/clone_id="NCI_CGAP_GCB1"
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/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGGCGCCCTCATTTTCTTTTCTTTT-
3']. Double-stranded cDNA was ligated to Eco RI adaptors

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TMAGE:713095"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/Note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I, Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
15'-TGTTCACATCGAAGTGGAGCGGCCGCCATTTTCTTTTCTTTT-
3'. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
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BASE COUNT      142 a      106 c      92 g      133 t
ORIGIN
Query Match      1.9%; Score 380.8; DB 31; Length 473;
Best Local Similarity 90.9%; Pred. No. 1.1e-33;
Matches 431; Conservative 0; Mismatches 32; Indels 11; Gaps 2;
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DB 1 TTTAGCTTATCTGTAATAAATCATACAGAAACATTATTAATTAATGATGTTTA 60
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QY 19572 gcttctctgcttaaaactaaataatagctcctaagaagaacattcatttactag 19631
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QY 19632 aggaatcataagtttaagaacttaaaacacttggcaatttaagacagatccaagat 19691
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DB 121 AGGATCTTAATAAAGCTTAACAACTTTGGCAATTGAAGACACGCCAAGAT 180
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QY 19692 gcaaatgcctggtgaatgatcaaatattccatctgcacattaaacaagaagctgtc 19751
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DB 181 GCAAGTCCCTGGCTGAATATGATCAAAATATTCATCTGCCTTTAAACAAATGCAATTGT 240
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QY 19752 tatgcttggacatggcagagcccatatgttccccccttcaataaagtgtctc 19811
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DB 361 AATAAGTCAGCCAGAGCTCTCTGCTAATATCCCAAGTCCCTGCGGGTAGCCCCCGAG 420
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QY 19922 ggcacatcagcctcgtctcccaacactaagttcaacttcatgtctcagcacaa 19975
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DB 421 GGCGGCTCAGCTCCGTC-CCTCAACTAGTTCATTCAATGCTCTCATAGGCA 473
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RESULT 11
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DEFINITION CITBI-EI-2522E11.TF CITBI-EI Homo sapiens genomic clone 2522E11,
genomic survey sequence.
ACCESSION AO277241
VERSION AO277241.1 GI:3903437
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 538)
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AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
JOURNAL Unpublished (1998)
COMMENT Other GSSs: CITBI-EI-2522E11.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0200
Email: mdamads@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
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/sex="male"
/cell_type="sperm"
/Note="Vector: pBeloBAC11; Site 1: EcoRI; Site 2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT      182 a      94 c      56 g      205 t      1 others
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Best Local Similarity 85.5%; Pred. No. 5.9e-33;
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DB 538 TGTGTATATATTAAAGNATATGAGCCCTCGAATGTAATAACTATTGAAGAAACAGTTT 479
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QY 19108 atgtcgaagtgatcataagaagaataatatacttctgttataaagaattagaagggtca 19167
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DB 478 ATGTTAAGCGGTGAAGAAAGTAATAATTAATCTTTGGTAAAGATTAAGAGGCA 419
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 19168 taagaatgtggaatttactacataaagaagttaaaaaaattatgtttgaagtta 19227
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 418 TAAGAAATGGGATTTTACTTACCTTAATAAGTTAAAAA-----ATTGTTTGAAGTTTA 363
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QY 19228 agcaagttttaaaatgttaattgtaaaaaaaatctgtgtgtaaaactaattagctaaag 19287
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 362 AGCAAGTTTGAATGTATATGCT-AAAGGAATTTCTGTGTGAACCATATTGGCTAAG 304
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QY 19288 ataaaaggtatcatccaatttctgtgaactgagcatlaaagtaaaatgcaaaagtt 19347
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DB 303 TTAAGGGGTGTCATCCAGTTTTCGTGAACCTGACATTAATAAAGCAACAAAGGT 244
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 19348 ttctctggaagcaccaactgctcttcaaaaaaatataaaaggttaaaagagctgt 19407
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DB 243 TTTTCTTAAGTACTAAGTCTGCTTTTAAACAAAATTAATGAAGCGTTAAGAAAGAGCTAT 184
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QY 19408 aaaaacttactatgtlcaacatgaaaaatgtgtaaaatgtctatagagtttatt 19467
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DB 183 AACAAATTTACCTTATGTCAGACATTAATAATTGATAATAATATGTCTACAAGTTTATT 124
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QY 19468 aaaaatgaattcaacatcaatacaatacaataaaggtaaaattagcttactgtga 19527
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DB 123 AAAATTGAAGTTTAACATTAATAGCACACATTAATAAAGGTGAATTTACTTATCGGTA 64
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 19528 taaaatcataagaagattataataataaaatggtgttagcttcttggtcctga 19587
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 63 T-AAATTCACACAGAGACATTATCAATAAATGAATGAGTGTGGCTTCTTGGTTTAA 5
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Oy	19588	aaac	19591	
Db	4	AAAC	1	
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ACCESSION	AQ316362			04-MAY-1999
VERSION	AQ316362.1			
KEYWORDS	GI:4047825			
SOURCE	GSS.			
ORGANISM	human.			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
TITLE	1 (bases 1 to 579)			
JOURNAL	Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.			
COMMENT	Use of human BAC End sequences for Sequence-Ready Map Building Unpublished (1998)			
	Other:GSS: RPCI11-107L20.TV			
	Contact: Shaying Zhao, William Nierman, Mark Adams			
	Department of Eukaryotic Genomics			
	The Institute for Genomic Research			
	9712 Medical Center Dr., Rockville, MD 20850			
	Tel: 301 838 0200			
	Fax: 301 838 0208			
	Email: hbeetlgr.org			
	Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong			
	(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html			
	Seq primer: SP6			
	Class: BAC ends.			
FEATURES				
Source	Location/Qualifiers			
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	/sex="Male"			
	/cell_type="Lymphocytes"			
	/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"			
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Best Local Similarity	84.7%: Pred. NO. 1.1e-32;			
Matches	466; Conservative 0; Mismatches 73; Indels 11; Gaps 4			
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Db	579	AATGATATATTTAAAGTAAATTTGGCCCTCCCTCAATGTANAACTATTGGAAGAAACACTTTA	520	
Oy	19109	tgtgcgaagtgcatagaagaagataaatactactttgtgtcaaaagattgaagagagcat	19168	
Db	519	TGTGCAAGCTGTGAAGGAAGTAATAATTTACTTTTGTGTAAGAAGTTTAAGAGGCA	460	
Oy	19169	aagaatgtgagattttacccatcataaagaaggttaaaaaaattatgttttgaaagttaa	19228	
Db	459	AAGAATATGAGATTTTACTACATTAATAAGGTTAAAAA---ATTATTTAAAGCTTTAA	404	
Oy	19229	gcaaattttaaaatgttaattttaaataaaatcttggtgtgaanaataatgtcraaga	19288	
Db	403	GCACCTTTTGAAACCTTAACCTGT-AATGGAATTTCTGTGTGTAACATATTTGGCTAAAGT	345	

QY	19289	taaaagatcatccoaagtttctgtgacggaacataaagtaaaatgcacaggt	19348
Db	344	TAAAGGGATATCCAGTTTCTTGTCTACCTGACGACATTTAAATTAACACACACAGTT	285
QY	19349	ttcttgaagcaccacacgtcctctttaaacaataataaaaggttaaaagtcgtga	19408
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QY	19409	aaaacttacctatgttcaacaatgaaaaattggataaataatgctataggttttata	19468
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QY	19469	aaattaagtttaacattataacacacaaataaagatgaaaaattagtttctgtat	19528
Db	164	AAATTGAGTTTACATTTATTAACACACTATATTAAGGTAATTAAGTTTATGCTTAT	105
QY	19529	aaaaatcacacaagaagtatttaaataaataatggttttagcttcttctgtctaaa	19588
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QY	19589	aactaataa 19598	
Db	45	AAACAAATA 36	
RESULT	13		
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LOCUS	Homo sapiens chromosome 11 clone PTWB59.14 map 11p15.5, genomic		
DEFINITION	survey sequence.		
ACCESSION	AF101960		
VERSION	AF101960.1	GI:4193786	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 2971)		
TITLE	Bepko, G., O'Brian, K.C., Kim, Y.C., Schreiber, G. and Pitterle, D.M.		
JOURNAL	A 1.4-Mb high-resolution physical map and contig of chromosome segment 11p15.5 and genes in the LOH1A metastasis suppressor region		
MEDLINE	Genomics 55 (2), 164-175 (1999)		
REFERENCE	2 (bases 1 to 2971)		
AUTHORS	Bepko, G., O'Brian, K.C., Kim, Y.C., Schreiber, G. and Pitterle, D.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-OCT-1998) Medicine and Radiology, Duke University Medical Center, Box 2610, MSRB, Room 117, Durham, NC 27710, USA		
FEATURES	Location/Qualifiers		
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	/note="part of a 1.4 megabase contig including the LOH1A metastasis suppressor region Bln T"		
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Best Local Similarity	71.9%: Pred. NO. 1.9e-31;		
Matches 537; Conservative 0; Mismatches 200; Indels 10; Gaps 5			
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Db	424	CAAAAACCCACAGCACAATATATATATATATATTTGTTATTTATTTATTTAT	483
QY	5157	tgcttttggagacgggtctccaccctcgttggccagagctgagatggaagtgtgac	5216
Db	484	TATTTTCCGAGACAGTGTCTACCT-CGTGTCGCCAGACTGGAGTGCAGTGGCACACT	542

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QY 5217 tagctgtcagcctcaacacctccctgtcgaagaacatccctccacctcagctccagc 5276
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543 TGGTCTACCTGCAACCTCCGGCTCTGGGTTTCAACGATTTCTCCCTCAGCTCCAG 602
QY 5277 taagtgtactacagcggtgtgcacacacacacccggtaattttgtatttttagtaga 5336
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603 TAGCTGGGATTACAGGGCGCCGCCACACACACAGCTAATTTTGTATTTTGTATAGAGA 662
QY 5337 ttgggttttgcattgttcagggaaggtctcaaccccttggtcgaagaacatccggccg 5396
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663 TGAGCTTTCACATGTTGGCCAGGCTGTCTCAACTCTCAGCTC--GTGATCACCACA 720
QY 5397 cctcagaagcccaagactgtggaattataggtgtggtggtccactgtggtccaaactct 5456
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721 CCTCAGGCTCCCAAAAGTGTGGATACAGGACATTAAGCCAGCAGCTGTGGCC---CAAC 776
QY 5457 ctcatataactagaatatagttatcaccctcaagaataacttaacttgtgtcggtacagt 5516
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777 ATATATATTTATGCTGAAGACTGAATGTTTCTAAGATCAGAAACAGCCAGCAGAGTG 836
QY 5517 gtccagcctgtatacccaagcattttgggaagccgaggtgggtggtacacaaagtccagga 5576
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837 GCTACCCCTGTATCTCTGGCAGCTTTGGAGAGCCGAGCGGCGAGATCAGAGGTCAAGA 896
QY 5577 gtccaagaccagcctgtgccaaggtgtgtgaaccccgctctctactaaatgtcaa--aaaa 5634
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897 GATGAGAACCATCTCTGGCTTAACAGCGTGAACCCCGTCTACTATAAATAATATAAATA 956
QY 5635 aattagtcagagcatgtgtggtcagttgtctgtatcccaatactcgtggaagctgtgagc--ag 5633
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957 AATTAGCTGGGTGACAGTGTGGGACCTGTAGTCCAGCTACTGGGAGGCTGAGGGGG 1016
QY 5694 agaatctgtgaaccccggaagcggaagcgtcaggtgagccagaatctgtccacagcagctc 5753
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1077 CAGCTTAGGGGACAGGGGAGACTTCGACTCATAAATAAATAAATAAATAAATAAATAAATA 1136
QY 5814 cttaagctactgtccatatacccaatt 5840
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RESULT 14
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DEFINITION H2_5571_B2_B12_T7A Rpci-11 Human Male BAC library Homo sapiens
ACCESSION A0752136
VERSION A0752136.1 GI:5539294
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 866)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

```

```

Clones are derived from the human BAC library Rpci-11. For BAC
library availability, please contact Pieter de Jong
(pieredejong.med.bufileo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bufileo.edu/ordering\_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1147 row: D column: 24
Seq primer: T7
Class: BAC ends
High quality sequence stop: 866.
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685 GACATCTGAACCTGTGTAACATCGTCTTGGAACTTGCCCACTCATNTNAGATGAGAGC 626
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625 ATGGCTGTATCACCACGAGC----- 605
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518 -GATACCTGATTTTGG--TTGTTCTGTGTGTGTAACCTTAAGAAGTGTGTGTGTC 462
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QY 18265 tcaagaagatttaaggtgagattacgtgttactatgaactagaagaactagaact 18324
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Dd	164	TCCCGTA 158	
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DEFINITION	Homo sapiens chromosome 11 clone pTWB59.14 map 11p15.5, genomic survey sequence.	GSS	08-MAR-1999
ACCESSION	AFI01960		
VERSION	AFI01960.1	GI:4193786	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
Eutheria; Primates; Catarrhini; Homidae; Homo.			
REFERENCE	1 (bases 1 to 2971)		
AUTHORS	Bepko,G., O'Brian,K.C., Kim,Y.-C., Schreiber,G. and Pitterle,D.M.		
TITLE	A 1.4-Mb high-resolution physical map and contig of chromosome segment 11p15.5 and genes in the LOH1A metastasis suppressor region		
JOURNAL	Genomics 55 (2), 164-175 (1999)		
MEDLINE	99134294		
REFERENCE	2 (bases 1 to 2971)		
AUTHORS	Bepko,G., O'Brian,K.C., Kim,Y.-C., Schreiber,G. and Pitterle,D.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-OCT-1998) Medicine and Radiology, Duke University Medical Center, Box 2610, MSRB, Room 117, Durham, NC 27710, USA		
FEATURES	Location/Qualifiers		
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	/note="part of a 1.4 megabase contig including the LOH1A metastasis suppressor region Bln T"		
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ORIGIN			747 t

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Db 839 AGCCACCTGCTGCGTGG - - -CTGTTTCTGATCTTATGAAAAATTCACGTCCTTTACCATATA 784

QY 5492 aacttaacatttgcctcgggcaacagtgtctcaagcccttgaatcccaagcattttggagcg 5555

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QY 5552 aggtgtgtgtgatcccaagttcaggaagtctcaagaccgccttgcgccaagtgtgtgaaaccc 5611

Db 723 AGGTGGGTGGATTCACGAGGTCAGAGGTTTGAGACCAAGCTCGGCCAATTTGTGAACCTTC 664

QY 5612 gctcttactaaaatgtcaaaaaaattatgcacagcatgtgttggaagtctgcttgaatccca 5677

Db 663 ATCTCTACTAAATAAT - - -ACMAAATATAGCTGTGTTGGTGGGGGCGCTGTAAATCCCA 607

QY 5672 gatactcggggagctcttgggca - gagaatttcttgaacccaaggaaggggagctctgaagta 5730

Db 606 GCTATTTTGGGAGCGCTGAAGCGCAGAGATTCCTTTGAACCCAGGAGGGGAGGTTTGCAGTGA 547

QY 5731 gccaaagatcgtgccaacatgcactccagcgttggggagacagagttgtctcaaaaaaataaaaaa 5790

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QY 5791 agaatt 5796

Db 486 ATAAAT 481

Search completed: February 28, 2000, 14:48:51
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2000, 08:44:14 : Search time 20117.6 Seconds
(without alignments)
-3767.414 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Searched: 821193 seqs, -1518192014 residues

Database: GenEmbl.*

Word size: 0

Number of hits that pass the threshold: 1642386

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49:	em_hum5.*

50: gb_pl3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	3992.2	16.0	135305	11	HSJ1112D6	AL080317 Human DNA
3	3544.4	14.2	227567	42	AC008554	AC008554 Homo sapi
4	3494	14.0	79376	11	HS454G6	298750 Human DNA s
5	3159.8	12.7	7728	11	AF058997	AF058997 Homo sapi
6	3082.6	12.3	137413	42	AC011036	AC011036 Homo sapi
7	2884.2	11.6	116679	32	HS0636H5	AL121602 Homo sapi
8	2879.4	11.5	162921	33	HSJ603114	AL122001 Homo sapi
9	2783.6	11.2	191235	42	AC012487	AC012487 Homo sapi
10	2647.2	10.6	163738	42	AC009505	AC009505 Homo sapi
11	2644.2	10.6	138088	43	AC010877	AC010877 Homo sapi
12	2559.6	10.3	144304	32	HS03383P5	AL121947 Homo sapi
13	2414	9.7	105363	11	AC003983	AC003983 Human PAC
14	2396.8	9.6	37139	40	AC006047	AC006047 Homo sapi
15	2386	9.6	100000	10	AP000509	AP000509 Homo sapi
16	2385	9.6	236822	10	D84394	D84394 Homo sapien
17	2385	9.6	110409	42	AC010487	AC010487 Homo sapi
18	2343.6	9.4	158463	44	AC011019	AC011019 Homo sapi
19	2342.6	9.4	123585	11	AC004707	AC004707 Homo sapi
20	2328	9.3	18226	11	HS46618	AL030998 Homo sapi
21	2317.8	9.3	167932	41	AC008697	AC008697 Homo sapi
22	2296.6	9.2	161428	41	AC009542	AC009542 Homo sapi
23	2294	9.2	174768	40	AC009330	AC009330 Homo sapi
24	2286	9.2	113853	40	AF196971	AF196971 Homo sapi
25	2270.6	9.1	213315	43	AC016047	AC016047 Homo sapi
26	2215.4	8.9	36921	40	AC004185	AC004185 Homo sapi
27	2133.2	8.5	196501	40	AC005908	AC005908 Homo sapi
28	2096.8	8.4	171636	10	HS215K18	283820 Human DNA s
29	2089.6	8.4	246240	5	AR036572	AR036572 Sequence
30	2089.6	8.4	246240	5	AR036573	AR036573 Sequence
31	2089.6	8.4	246240	5	AR036574	AR036574 Sequence
32	1991.2	8.0	203488	42	AC009488	AC009488 Homo sapi
33	1991.2	8.0	173157	42	AC011895	AC011895 Homo sapi
34	1965.6	7.9	132805	11	HS339A18	297054 Human DNA s
35	1943.2	7.8	114330	40	AC004772	AC004772 Homo sapi
36	1868.4	7.5	226345	40	AC005406	AC005406 Homo sapi
37	1860.6	7.5	164285	42	AC009703	AC009703 Homo sapi
38	1709.2	6.8	268399	33	AC004469	AC004469 Homo sapi
39	1700.8	6.8	200607	44	AC016775	AC016775 Homo sapi
40	1589.4	6.4	112184	11	AC004054	AC004054 Homo sapi
41	1586.2	6.4	141672	10	HS142P18	AL031073 Human DNA
42	1556.2	6.2	179905	42	AC011751	AC011751 Homo sapi
43	1491	6.0	191079	33	HS1036D20	AL109851 Homo sapi
44	1470	5.9	158810	44	AC011604	AC011604 Homo sapi
45	1424	5.7	114638	11	HS799N4	AL022147 Human DNA

ALIGNMENTS

RESULT 1

HS295C6	102258 bp	DNA	PRI	23-NOV-1999
LOCUS	Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains ESTs, CA repeat, STS and Cpg island.			
DEFINITION	297876			
ACCESSION	297876.1	GI:2582745		
VERSION	1q24; Cpg island; repeat polymorphism.			
KEYWORDS	human.			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			

REFERENCE 1 (bases 1 to 102258)
AUTHORS Grafham,D.
TITLE Direct Submission
JOURNAL Submitted (27-OCT-1997) Chromosome 1 Project Group
(http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Nov 2, 1997 this sequence version replaced gi:2465042.
IMPORTANT: This sequence is the entire insert of clone 295C6.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variations annotated may not be found in the sequence submission
corresponding to the overlapping clone as we submit sequences with
only a small overlap as described above.
This sequence was generated from part of bacterial clone configs of
human chromosome 1, constructed by the Sanger Centre chromosome 1
mapping group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1/
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key
The true left end of clone 295C6 is at 1 in this sequence. The true
right end of clone 295C6 is at 102258.
295C6 is from the library RPCII constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/
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/clone_1lb="RPCT-1"
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1375..1683
/note="AluSp repeat: matches 303. .1 of consensus"
repeat_region
2028..2310
/note="AluSg repeat: matches 300. .1 of consensus"
repeat_region
2612..2903
/note="AluSg repeat: matches 301. .1 of consensus"
complement(4475..4866)
/note="match: 223618 STS containing (CA) repeat"
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4625..4670
/note="23 copies of GT 100 & conserved; differs from
223618"
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4766..4897
/note="MIR2 repeat: matches 145. .1 of consensus"
repeat_region
4969..5140
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5146..5448
/note="AluDo repeat: matches 302. .1 of consensus"
5503..5795
/note="AluSg repeat: matches 1. .299 of consensus"
5797..5925
/note="MER42c repeat: matches 1265. .1124 of consensus"
5923..6039
/note="LIMB6 repeat: matches 920. .804 of consensus"
6123..6415
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7799..8099
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9002..9302
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9692..9983
/note="AluDo repeat: matches 1. .301 of consensus"
10986..11071
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repeat_region
13907..13973
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13975..14489
/note="MER1a repeat: matches 526. .1 of consensus"
repeat_region
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16144..16585
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17173..17534
/note="LTR2 repeat: matches 105. .449 of consensus"
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AA077391"
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/note="3 copies of 39 mer 81 & conserved"
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T62974 AA283144; match: T57835 F00049 N75628 AA382351
AA300207; match: M37181 N52820 AA337459 M87851 H84729;
similar to endogenous retrovirus POL POLyPROTEIN"
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/note="match: multiple ESTs; match: AA401243 AA258918
AA248892 AA096209 R36280"
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repeat_region
26752..27050
/note="AluSg repeat: matches 1. .299 of consensus"
repeat_region
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/note="AluSg repeat: matches 1. .303 of consensus"
repeat_region
28316..29066
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repeat_region
29937..30237
/note="AluSg repeat: matches 1. .301 of consensus"
repeat_region
30238..30315
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31289..31379
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31479..31525
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36692..36944
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repeat_region 40769..41662
repeat_region 41764..42556
repeat_region 42557..42857
repeat_region 42876..43925
repeat_region 44235..44498
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repeat_region 44933..45220
repeat_region 45304..45336
unare 45337..45637
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repeat_region 46817..46935
repeat_region 47393..47677
repeat_region 48309..48404
repeat_region 48620..48862
repeat_region 48865..49159
repeat_region 51182..51467
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 24961; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 tttaaataataatggaataatgaggttgaagaagagctgtctctcatatt 120
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DB 15240 TTTCTAGTCTCTACTGCCACCTATATACACCAATAGCAAGCCACTACCCCATCAAGT 15299
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DB 15300 CATGACCTCTGACTGGAGGCTCCCATTTGCTTAACGAGCATGAACCAAGGCTCTTTATG 15359

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DB 15360 TGACACACAGACTTTCAAAGCTCATTTATCTTTCTTCCACTCTCTCCATGCA 15419
QY 421 tctacccttccacaacagaagcaggttagaggttccctgcaacaccagaagctattctcc 480
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DB 16380 TTCTCAAGGCCATCTTTTGAAGACACCAAGATGGCCAGCAACACAGAGTATGAGGTG 16439
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OY	4141	cttttggttaaaaaagataagaaggagcgataagaatgtggaatttttaacctataaaga	4200
Db	19140	CTTTTGTTAAAGATTAAGAAGAGGCAATAAGATGTGATTTTAACTACATTAATAAG	19199
OY	4201	ttaaaaaaattctgttttgaagaagtttaagcaagttttaaatgttaatttgcataaaaaa	4260
Db	19200	TTAAAAAATTTTGTTTGAAAGTTTAAGCAAGTTTAAATGTAAATTTGTAATAAAAAA	19259
OY	4261	attcctgtgttaacaaacttaagctaaagaataaaagttatccagtttctcgtgaaac	4320
Db	19260	ATTCTGTGTAACTAATTAATTAAGTATAAAGTATAAAGTATCACTTTCTGTGAAC	19319
OY	4321	tggacataaagtaaaaaatgcacacaggtttctctgaaagcaccaactgcctttaaca	4380
Db	19320	TGGACATTAATAATTAATAAAGCAACAGGTTTTCTTGAAACACCAACTCTCTTTAACAA	19379
OY	4381	aaatataaagaagtttaaaaaagctctgttaaaacttaactctgtgtcaaacgtaaaaat	4440
Db	19380	AAATTAATAAAGTTAAAAAGCTCTGTAATAACTTAACCTTAATGGCAACAATGAAAAAT	19439
OY	4441	tggatcaaatatgctatagaggttcttaaaaaatgaagtttaacatataacaactaat	4500
Db	19440	TGGATTAATATGTCTATAGAGGTTTTATTAATAATTAAGTTAACTTAATAACACACTAAT	19499
OY	4501	ataaaggtaaaaattagcttatctggtlataaaaaatcatacaagaagttatataatata	4560
Db	19500	ATTAAGGTAAAAATTTAGCTTAATCTGTTATTAATAAATCATCAAGAAGTATTATTAATATA	19559
OY	4561	aaatggtgttaggccttctgtgtctaaaaaactaataaaataggtctcctaaaggaaact	4620
Db	19560	AAATGGTGTTTAGCTTTCTTGCTCAAAAACTAATAAAAAATGAGCTCAAAAGGAACAT	19619
OY	4621	tcaatttcaactagagatcatagaagttlaaagacttaaaacaaacttggcacaataagaca	4680
Db	19620	TCATTTTACTAGAGATCATAGAAGTTAAAGCTTAAACAACAACCTTGCAATTAAGACA	19679
Db	4681	gcatacccaagatgcacaaatgcctcgtgttgtaaaatggaatcaaatatccaatctgcacattaac	4740
Db	19680	GCATTCACAGAATGCAAAATGCCGCTGTGAATGTGATCAAAATATTCATCTGCACATTAAAC	19739

QY	474.1	aaagcaggttgtagtgcttctgacacgtgcagcagagccctatgtcccttcca	4800
Db	19740	AAAAGCAGTGTATGCTTGTGCACATGGCAGGCCAGAGCCCTATTGTCCCTTCCA	1979
QY	480.1	ctaagtgatctcccaatcccaacagcgtgvggcctgcaltgtagctctttccagatctc	4860
Db	19800	CTAAGTGTGTCTCCANCTCCACGAGCGTGGCTGTGATGTAGCTCTTTCAGAGATTCT	1985
QY	486.1	acagcctggagtaataagtcatgccaactctctctgtatccctgtggtcagcccg	4920
Db	19860	ACAGCTGGAGTATATAGTATCTATCCAAACTCTCTGTCTATCCCTGTGGGTACCCCCG	1991
QY	492.1	agggccatccagccctccgtctcccaacactaaagttaactctatgctctcaacagaa	4980
Db	19920	AGGGCATCCAGCCTCCGTCTCCCAACTAAGTTCCTTCAATGTCTTCACCAAGAGA	1997
QY	498.1	ggaaccttaggattctctcttgagacccctgaagtgatgcataagctaaagatttcaaag	5040
Db	19980	GGAACTTAGGATTCTCTTGAGACGCTGAAGTGATGTAAGACTTAAGATTTTCAAGAG	2003
QY	504.1	cttatcaatcagtcagccctgtgtcatcccaagcgagatgvtggtgtattgtgtgga	5100
Db	20040	CTTATCATCATAGTCAGCCCTTGTTCATCCCCAAAGGAGATGTGTGTGATTGTGGGA	2009
QY	510.1	ccttacttgagcaactctgcgcgaaataacttgagtgcaacttaactatgctcagttgct	5160
Db	20100	CCTTTACTGGGCATCTGCGGAATTAATCGAGTGGCACTTATACTTGTAGTCAAGTGGCT	2015
QY	516.1	atcccttcaacccttgatcttcaacaagaaggaggaazaaataagacatcgtaaacg	5220
Db	20160	ATCCCTTCAACCCGTGGCATTTTCATCAACAAGAGGGAGGAAAAATAGACATCGTAAAGCG	2021
QY	522.1	agagaagcccccctatagtgcttctcgactctcaagtcacgttaagcgaattggaatccc	5280
Db	20220	AGAGAACCCCCCTTATAGGTCCTTTCACACTCTACGTCATTTAGACGAATTTGAGTCCC	2027
QY	528.1	acgaggaatccagatcaatctttaaagcttgaaataaataagtgataaataatttaagtaat	5340
Db	20280	ACGAGGAATCCAGATCAATTTAAACCTTGAATCAAAATAGCTACAAAATTTTAAGTCAT	2033
QY	534.1	attcttagtgatgtagtgcataaaatgtaaaatgtaataatatactatatacaaca	5400
Db	20340	ATTTTACTGAGTGTATGTTATTAATAATGTAAATTTAGTAAATATATATTACAAACA	2039
QY	540.1	cagcaacaagccttctcatgagtgtgaaagaaaaactcaggtcgccccagccctvgggcta	5460
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QY	546.1	ccgtactgcagaaagtgtgcacactctcatgtgcccaaaaaaataaaaaaaggcca	5520
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QY	552.1	ctctatcaaatcttaagatctaatttagacataacaagagctctactcatatgacaagataat	5580
Db	20520	CTCTATCCAAATTTCTAAGTTAATTTAGACTTAACCAAGGCTTTCATATGCAAAAGATTAAT	2057
QY	558.1	tgaatcccaactcaagaagtttcaacaagaagtaaaagtgtgtcaaaagttaacagtg	5640
Db	20580	TGAATCCCAACTTCAAGGTTTCAACAANAAGTAAAGTTTGCTAAAGTTAACAGTGT	2063
QY	564.1	aacatgattatagtaactcttaactctgtgtgaccttagacagtcagtcacagataaa	5700
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QY	570.1	agaaagttcacttaaaaaaataaaagaatgtgtctcttcaaaaaaataaaatgca	5760
Db	20700	AGAAAGTTCACCTTAAAAAATAAAAAAAGATGGTTATCTTCAAAAAAATAAATGGCA	2075
QY	576.1	gttgagatttcaaccagactcagggcctctgcacaagcgacgtgcctatctctcaaa	5820
Db	20760	GTTGGAGTTTAAACCCAGACTGTAGGGGCTGTGGCCAAAGGCCAGTGTGCTATCTCTCAAA	2081
QY	582.1	caactaagtgggtttcccaaaagctgccccccatactaaagggccctgycagcaagggcc	5880

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Db 20880 CTGTTAGACACAAGAGCAGATTAAGCTTAACCTTAGGCAAAACCTTAACCTTAAGTCCCCC 20939
Qy 5941 ccatgctgtgtgactttaatcagtlaccaaagacatcatagtaactgaatgctagact 6000
Db 20940 CCATCTGTGGTGGACTTTAATATAGTACCAAGACATCTTTAGCTATATCATATGCTAGACT 20999
Qy 6001 aactagataccaaagctgtctctgtgaaaaatccccaataacatltgaagtttgacaac 6060
Db 21000 AACTTGATATCCAAACCTTGCTGTGAAAAATCCCAATTAACCATTAAGTTTGCAACAC 21059
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Oy 20701 aggcctagagaaattcaatgacttgccttaagcttccacagctcgggaatccttggggcaatgt 20760
Db 35700 AGGCTCAGAAAGTTCATATGACTTGTCTAACTCTCAAGCTGGGAAATCTTTGGGCACTGT 35759
Oy 20761 ctgcaagacacgaagaagcttctcttagatctctacacttcttctatgatacccatg 20820
Db 35760 CTGCAMACACGAAGAGCTGTCTTAGATCTTACACTTTTCTTATATATACCAATGG 35819
Oy 20821 gtccaglatgaaagagttacttggagacacagagcttgaaglaa tcccttccagaaactcc 20880
Db 35820 GTCCAGTATTGAAGAGTACTGGAGACACAGGCTGGAAGTATCCCTTTCCAGAACTCC 35879
Oy 20881 catagcagaagttagttcgtctcatalagaaatgcatgcttccgtcgtgtgttcaat 20940
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Oy 20941 atatgttatacatctctcgtccagccctagcttcttcttataagaaatgctcag 21000
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Oy 21001 taaatgcttgtgaattagtgagtgagtgagtgaggcagtaactaaagtgcctcttt 21060
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Oy 21061 taatacaaaagaaattgagatgggaatacactctcatalatgcatctgtgtgcaattc 21120
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Oy 21121 gtccatcacacttcttctcgaattgattgaagaacaggtgaagaacccgggtgcagttg 21180
Db 36120 GTTCATCACAATCACTTTCTCTGAATTTGATTAAAGAACAGTAAAGCAGGTGACAGTGG 36179
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QY 21181 ctcatctcgtaatcccaagcactttggagccgagcgaggtgagctacacttgaagtcagg 21240
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Db 36180 ctcatccctgtatcccaagcactttggagccgagcgaggtgagctacacttgaagtcagg 36239
QY 21241 aattcgaagcccccgcgcgcgaacatgacgaacactcactcactaataataaataaatt 21300
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QY 21301 agccaggtgtgtgtgagcagatgctgtacacagcactcagaagagctgagtaagaagaa 21360
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Db 37320 tctattctcaacaaagtgtgctgtcagtagaagtagcctaaacataatgttaggttccca 37379
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Db 37380 tcccatagttcaacttactgttcaaacatgaaagccttatgtattgtgaccttgaaaga 37439
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Db 37680 gggaaatgtctaacctcagaaatgggtgagtagcaaatgaaacagagccagcatgtcctgaagt 37739
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Db 37860 atgtcaataaggaaataactcgtcttcttggcctcctatctttaaataaaatctaa 37919
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Db 38040 caagcattatccctgtgttcaaaaacaaatccaatatactcctttagttatttttaaa 38099
QY 23101 tgtatgtgttagttagtccgtctcctccactgttaaaagaaactcagtagtggtaatt 23160
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Db 38100 tgtatgtgttagttagtccgtctcctccactgtgttaaaagaaactcagtagtggtaatt 38159
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Db 38160 ttaacaagaaagaggtttaattagtagcaggttcaatgagcgtgtagcagagagcagtagct 38219
QY 23221 gggagagactcaactataatagcagaagaagagagagagagagagagagagagagagag 23280
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Db 38220 gggagagactcaactataatagcagaagaagagagagagagagagagagagagagagagag 38279
QY 23281 ggcag 23340
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Db 38280 ggcag 38339
QY 23341 catcactatcagagaaacagagagtagtaatacaccctatgatacactcactca 23400

D	38340	CATTACATATCAGAGAACGAGAAAGGATATATCCACCCTATGATCCATACACTCCTA	38399
O	23401	ccagtcctcccccacacacacatttgggagataataatcaacatgagatttggaggagataca	23460
D	38400	CCAGTCGCCCTCCACCAACATTGGGATTAATATTCACAAATGAGATTGGAGAGGATACA	38459
O	23461	aatccaacacatacaaatgaataaatttttttactatagttaccggttggtaactga	23520
D	38460	AATCCAAACCATATCAATGAATAAATTAATTTTAATCTATAGTTACCCTGTTGTAATGCA	38519
O	23521	aatactaggtcttctcatctctctctcttcttttttactacatctgacaccccacattcct	23580
D	38520	AATACTAGGTCTTCTCATTTCTTCTCTTTTGTGTAGCATGACACGCCCAATTCCT	38579
O	23581	cctcatccccacatacccttcccagcctttggtaacacatctatatctctataccccat	23640
D	38580	CCTCATCCCCCCTACCTACCCCTCCACGCTTGGTAACTATCTAATTTCTTACCCCAT	38639
O	23641	ggattcaatcatattaaatttttttttttttttttttttttggagcggagctgcctcgttg	23700
D	38640	GAGTTCATCATTTTAATTTTTTTTTTTTTTTTTTTGTGAGACGAGATCTCGCTGTG	38699
O	23701	ctcaggctggagatgtagtggcgagatctgcgtcactgcgaacctgcctgcctgggttca	23760
D	38700	CTCAGGCTGAGATGACAGTGGCGCGATCTGGCTCACTGGAACCTCTGCTCTGGGTTCA	38759
O	23761	agcgattctctgcctcagcttccagagtactgtgatttgcaggacatgcacacacatgcc	23820
D	38760	AACGATTCCTCGCTCGCTCAGCTTCAGAGATGCTGGGATGTCAGGCAATCACACCATGCC	38819
O	23821	tggccaatttttgtaatttttagtaagcgggggttctgactgtgttagtcagaactgtctc	23880
D	38820	TGGCTAATTTTGTATTTTATTTAGTAAAGACGGGGTTTCACTGTGTTAGTCAGACTGTCTC	38879
O	23881	gaactccttgaccatctgaatctgcctgccttggcctcccaagttgtcggattacagcgat	23940
D	38880	GAATCTCTGACTCATGATCTGCTTGCTTGCCCTCCCAAAGTCTGGGATTTACAGCAT	38939
O	23941	gagccacacatgcacagcccacatagtttaatttttagcttccacacaataagtagaacat	24000
D	38940	GAGCCACCATGCCCCAGCCCAATAGTTTAATTTTACGCTCCACAAATTAAGAGAAACAT	38999
O	24001	gtgggttctctttctatcacctcgtgttatttttaactaatatagccccacttccaccc	24060
D	39000	GtGGTTCCTCTTATACCTGGGTTTAATTTCACTTAATATATGACTCCATTCCTCATCC	39059
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D	39060	ACGTGTGTGCAATGACAGATCTATTTTTTTATAGCTGAATAGTACTTGTGTGTAT	39119
O	24121	atgtacacatttcttataccattctctgttgaatgacacttaagctgtgttccaaagtc	24180
D	39120	ATGTACCAATTTTCTTATCCATTTCTGTGTATGACACTTAAGCTGCTTCAAGTC	39179
O	24181	ttgactactgtgaatagcacctgcgcagtaaacatgggaagtgtagtacctcttcataataat	24240
D	39180	TTGACTACTGTGAATAGCACTGCAGTAACATGAGAGGTGTCTTCTTCAATATATT	39239
O	24241	gatttccttctcttggatgatagtactcgaaggatgaattctcagatttatggtagcct	24300
D	39240	GATTTCCTTCTTGTGATATGTATCTAGGAGATAAATTTCTAGATTATATGATAGCTCT	39299
O	24301	atttttagcttttgaagaaacttcaaacgtgtcccaagttggctgtgctaaattactt	24360
D	39300	ATTTTACTTTTATGAGAACTTCAAACTGTCTCCAAAGGGCTGTGCTAATTTACTT	39359
O	24361	tctcataacagtgtagacaagattccctttttccacatccctgtccagcgtttgttatgt	24420
D	39360	TCTCATTAACAGTGTACAAAGGATTCCTTTTTCACATCTCGTCCAGCGTTTGTATATG	39419
O	24421	cctgtccttttggataaaagtcattttaaactcggggtgaagatgataatcttatgttagtttc	24480

Db	39420	CCGNCCTTTGGATAAAGTCATTTTAACCTGGGGTAAGATGATATCTATGTGATTTT	39479
QY	24481	gatttccatttactcgaatgatgtgagatgttgcacctttccaatattttccataac	24540
Db	39480	GATTTTCATTATTCGATGATGATGGATGGATGTGTGCACCTTTTCACATATTTTTCACATAC	39539
QY	24541	tgttttcgacatttgaatgctcttcctttgaaaatgtcatttcgaatctcttttttttgag	24600
Db	39540	TGTATTGCATTTGATGACTCTCTTGAGAAATGTATTTGCATCTTTTTTTGTAG	39599
QY	24601	acggagcttcaactctgttaacctgggtctggatgtgcagtgtgcacattcaatctcacgaac	24660
Db	39600	ACGGAGTCTCATCTGTATACCTGGGCTGGAGTGCAGTGGACATCTCATCTACATGCACAC	39659
QY	24661	ctccagctcccttggatgttcaagtatctctgttcctaaagccctgaatgaactgtgatatagag	24720
Db	39660	CTCCGCTCCTCGGTGTTCAAGTATTCGTGTGCCCTCAGGCCCTGAGTAAGCTGGATGGATTACAG	39719
QY	24721	ggcgccacacacacagccccaagctcaattttttgatttttaagtagaagaggggtttcacat	24780
Db	39720	GGCGCCACACACTACGCCCAAGCTAATTTTGTATTTTAGTAGAACGGGGTTTACCAT	39779
QY	24781	gttggccagagctgtgcttctgaactcctgtactctgttacttggccacactgcgcctcccaag	24840
Db	39780	GTTGGCCAGGCGTGGCTTGAACTCTGTATCTGTATCTGTACTTGGCCACCTCGGCCTCCCAAG	39839
QY	24841	tgtctggattaaagctgtgagagcaatgtgcctgcgacctattccaagcctttacccattt	24900
Db	39840	TGCTGGGATTCAGCTGTGAGGCCACTGTGGCCCTGCTTATTCAGCTTTTATCCATTTT	39899
QY	24901	ttaatccaatatataagatttttttctatagaagctgttacaactctcttatalagagatgtt	24960
Db	39900	TTAATCAGATATTATGATTTTCTTATATAGAGCTGTACAGTCTTATATATGGAGTGTG	39959
QY	24961	a 24961	
Db	39960	A 39960	

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS
HS11112D6/c	Human DNA sequence from clone 1112D6 on chromosome 6q21-22.2, complete sequence.	AL080317 AL080317.11 GI:5830430	HGC: CPG Island. human.	SOURCE
ORGANISM	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	1 (bases 1 to 135305)	Patel,R.
REFERENCE	Direct Submission			
TITLE	Submitted (09-SEP-1999) Sanger Centre, Hinxton, Cambridgeshire,			
JOURNAL	CBI1 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk			
AUTHORS	On Sep 6, 1999 this sequence version replaced gi:5791529.			
COMMENT	During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.			
	The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:			
	Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORPEP. Information on the WORPEP database can be found at			
	http://www.sanger.ac.uk/Projects/C_elegans/worpep This sequence is the entire insert of clone 1112D6. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat			

HSJ11226 135305 bp DNA PRI 23-NOV-1999
 Human DNA sequence from clone 1112D6 on chromosome 6q21-22.2,
 complete sequence.
 AL080317
 AL080317.11 GI:5830430
 HTG: CpG island.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 1 (bases 1 to 135305)
 Patel, R.
 Direct Submission
 Submitted (09-SEP-1999) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk
 On Sep 6, 1999 this sequence version replaced gi:5791529.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Emi, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
 on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence has been finished
 according to sequence map criteria as follows. An attempt is made
 to resolve all sequencing problems, such as compressions and
 repeats, but not necessarily within known annotated human repeat

QY	6021	tcctgtgaaaatcccccaataaccccttaagaatttcgaacacccttaaccccgcaacttgc	6080
Db	30249	TCCTGTGAAAATCCCCGGCATTAACCTTGAAAGTTTGCAACACCCTTAACCCGGCACCTTAC	30190
QY	6081	tcctcgtatccagagagcccaagttaaacaatacctgtgtgaagctgttgactcaattatc	6140
Db	30189	TCCTGTGATCAGAGAGCCCACTTAAACATACTGCTGTGAGAGTATTGGACACAGTTTATT	30130
QY	6141	ctagttggcccaacctccaataacatccttaacaatacgtataactcgtgaagctgtacggtg	6200
Db	30129	CTACAGAGCCCCAACCCGAGACCAACCCCTTAACATCATGCTGAGACTGGAGTTGGACGTAG	30070
QY	6201	atgggagcagctttccaacacctctgcgaagctacga-----aaaagccctgttc	6252
Db	30069	ATAGAGACAGCTTTGGCCAAACCCCTGTCAAAAGTACTGTGAAGAGACGACAAAGCCCGGCC	30010
QY	6253	cagtcacaccccggaagctgtacgtgtccacgcgcgcgcgaagcattgagaaaactcaacg	6312
Db	29949	GGACCCATTTCTTAAATTTGGACTTGAACAGTAAGAGACTTCCACTGACCTTCCTAG	29890
QY	6373	actgagaacgtttcccaagtatacatcaagctcaagctcgtgtgtagaacaagaattgtaca	6432
Db	29889	ACTGATTAACCTTTCCGATATATACATTAATGACTGAGGTAGGACAAAGATTGCTACA	29830
QY	6433	gtccatattattcattgtgtattataagtgtaacgaagactcaaaagaacctgttgtat	6492
Db	29829	GTCCATATTATTATTAGGTTATTATAGGTACCGGAGCTCTAAAGAAACTTGTGTGAT	29770
QY	6493	aatgtctattctatccaaggtatgtacgcttagagaaataaccaactgtatgtgtatgac	6552
Db	29769	AATGCTATTCTATCTCAAGGTATGACGCCCCAGGATAACAACCTGATCGCTATTATGAC	29710
QY	6553	ccattttaagctcccaatgatacagcttttctaataataataaagagactgtgcccttct	6612
Db	29709	CCATTTTAAGCCTCCCACTGCTCACAGTTTTAAAAATAAATAAGACACTGGCTCTTTCT	29650
QY	6613	aggtgcacacaagtaagtaatagctaaagacagaagaagagatcccccaacatgtatcac	6672
Db	29649	AGGTGACACAGGTAAAGGTAAATAGCTAGACAGAAAGAAAGAGGCCCAAAAGTAATAC	29590
QY	6673	actaaaatttaagctgtgtgcccatataatagcaatcgcgatgaaataagatgcggttc	6732
Db	29589	CTTAAATTTTACGCCCTGTGCCGCTATTAAATAGTAACAGATGGGATAGGATGGGTTTC	29530
QY	6733	tttaaacctgaaaaaanaaaagttacacagcagaagaaataagtatatctgtccacgaattaa	6792
Db	29529	TCTGTGATTG---AAAAAAAAGTTTACACAGACGAGAAAATAAGTACTCTGTCTAAAAATAT	29474
QY	6793	gtctacgtgcacaatgtgtgtataactcgtctgtgtcatcctagctacttagaaaaag	6852
Db	29473	ATTATATG---AGATGHTGTCATAATCTAGTCTGHTGTCATTAGGCTACTTAAAGAAAG	29417
QY	6853	atgaaaaaagaccctgttagcttc--aaaaaggaagagccgcccctccttagagatg	6910
Db	29416	ATAAAAAATATCCGTGTTGGCTCCAAAAAAAAGAAAATCATGAGCCCTCTCCACAGTAG	29357
QY	6911	aagctgcacacccttgaattagtaattacaatcccttaaacccgaagtgtgaanaaag	6970
Db	29356	GAGCTGCACACCTTTAGATTGATATACAAACCCCTCAGACCCCAAGTAATAAATAAA	29297
QY	6971	aagtaacgtaatctctcgtggcgtcgataaaaaagacatagatcctagaaataacttag	7030
Db	29296	AAAGATATATGATACATTAGGCAATTGATGTGAAAAAGGACTGATCTCTGTATAGCACTTAA	29237
QY	7091	taaaagaggaggttcgtbaactctctcggaaacggtatttcaaaccttcataatcac	7090
Db	29236	TAAAGGAGAGGTTCAAAAGCGCTCTCCAGAACAGTATTTCAGACTTTCTATATGATAAC	29177

[illegible]

[illegible]

*	is not known and their order in this sequence
*	arbitrary. Gaps between the contigs are repre-
*	sents of N, but the exact sizes of the gaps are
*	not known. This record will be updated with the finished
*	sequence as soon as it is available and the accession
*	number will be provided.
*	
*	1 318: contig of 318 bp in length
*	
*	319 886: contig of 568 bp in length
*	
*	887 1782: contig of 896 bp in length
*	
*	1783 2247: contig of 465 bp in length
*	
*	2248 2470: contig of 223 bp in length
*	
*	2471 2638: contig of 168 bp in length
*	
*	2639 3193: contig of 555 bp in length
*	
*	3194 3926: contig of 733 bp in length
*	
*	3927 4631: contig of 705 bp in length
*	
*	4632 5675: contig of 1044 bp in length
*	
*	5676 6189: contig of 514 bp in length
*	
*	6190 7038: contig of 849 bp in length
*	
*	7039 7992: contig of 954 bp in length
*	
*	7993 8501: contig of 509 bp in length
*	
*	8502 9192: contig of 691 bp in length
*	
*	9193 9921: contig of 729 bp in length
*	
*	9922 10917: contig of 996 bp in length
*	
*	10918 11570: contig of 653 bp in length
*	
*	11571 12394: contig of 824 bp in length
*	
*	12395 12821: contig of 427 bp in length
*	
*	12822 13086: contig of 265 bp in length
*	
*	13087 13927: contig of 841 bp in length
*	
*	13928 14388: contig of 461 bp in length
*	
*	14389 14980: contig of 592 bp in length
*	
*	14981 15641: contig of 661 bp in length
*	
*	15642 16058: contig of 417 bp in length
*	
*	16059 16503: contig of 445 bp in length
*	
*	16504 16857: contig of 354 bp in length
*	
*	16858 17470: contig of 613 bp in length
*	
*	17471 18225: contig of 755 bp in length
*	
*	18226 18896: contig of 671 bp in length
*	
*	18897 20001: contig of 1105 bp in length
*	
*	20002 20423: contig of 422 bp in length
*	
*	20424 21074: contig of 651 bp in length

* 21075 21636: gap of unknown length
* 21637 22482: contig of 562 bp in length
* 22483 22741: gap of unknown length
* 22742 23249: gap of unknown length
* 23250 23909: gap of unknown length
* 23910 24765: gap of unknown length
* 24766 25961: gap of unknown length
* 25962 26615: gap of unknown length
* 26616 27017: gap of unknown length
* 27018 27743: gap of unknown length
* 27744 28040: gap of unknown length
* 28041 28179: gap of unknown length
* 28180 28252: gap of unknown length
* 28253 28427: gap of unknown length
* 28428 28839: gap of unknown length
* 28840 29813: gap of unknown length
* 29814 30571: gap of unknown length
* 30572 30791: gap of unknown length
* 30792 31200: gap of unknown length
* 31201 32938: gap of unknown length
* 32939 33652: gap of unknown length
* 33653 35495: gap of unknown length
* 35496 36439: gap of unknown length
* 36440 38042: gap of unknown length
* 38043 39886: gap of unknown length
* 39887 40124: gap of unknown length
* 40125 41094: gap of unknown length
* 41095 41832: gap of unknown length
* 41833 43389: gap of unknown length
* 43390 43514: gap of unknown length
* 43515 43635: gap of unknown length
* 43636 44810: gap of unknown length
* 44811 44866: gap of unknown length
* 44867 45042: gap of unknown length
* 45043 45856: gap of unknown length
* 45857 47270: gap of unknown length

47271 49182: contig of 1912 bp in length
* 49183 50454: gap of unknown length
* 50455 51456: gap of unknown length
* 51457 52173: gap of unknown length
* 52174 53707: gap of unknown length
* 53708 54471: gap of unknown length
* 54472 55278: gap of unknown length
* 55279 55974: gap of unknown length
* 55975 57736: gap of unknown length
* 57737 59997: gap of unknown length
* 59998 60515: gap of unknown length
* 60516 61770: gap of unknown length
* 61771 63584: gap of unknown length
* 63585 64278: gap of unknown length
* 64279 65874: gap of unknown length
* 65875 68179: gap of unknown length

Query Match 14.2% Score 3544.4; DB 42; Length 227567;
Best Local Similarity 76.0%; Pred. No. 0;
Matches 5306; Conservative 0; Mismatches 1166; Indels 512; Gaps 55;

QY 1986 aatccaaagacatcttatctctatccagcttagacctaagtgatgtaactagta 2045
DB 201285 ACTCCAGAGTCGCCACCCATCTTGACAGATGAGAGATCTCTATAAATTGGCC 201226
QY 2046 ttccctgttgaagagacagaccctcatalgttttactcagaaga--- 2102
DB 201225 CCTCTGGTGAAGAGAGAGACCCCTCATATTGTTTATCTACAGTAC 201166
QY 2102 -----aagaagaatgaataaagca--gatagccggcgcttagaaccagccg 2152
DB 201165 CTGTTTAAAGAAAAAACAAGAGATGAATCAAGACAGCGCCGACGCCCA 201106
QY 2153 aaaccagggctgggctgctgactaagctcgatgtaaatccgaccctgacctag 2212
DB 201105 AAACCAAGCCCTGGGCTGCTGCTTAACCTAGTAGTTAAAAATCACTTAAC 201046
QY 2213 caactgtgtatctatagatccagacattgtatgaaggcattgtatgaagaacat 2272
DB 201045 AATCAATGTATTTGATAGATTCAGCA-----CATGTATAGAGAACAC 201001
QY 2273 tgtgaatctctcgctgtgttctgttcaactgtgacacaggtgtcagaccctgtca 2332
DB 201000 TGTGAATCTCCCGCCCTGTTCTCTCCCTGACCACTGGTGATGACGCCCTGTCA 200941
QY 2333 cgtaccctgtgcttaactaatcgaatccacccctcattcagggccttagagttgt 2392
DB 200940 CATTA-CCCTTCTGTTTCAATCAATCATGACCTTTTCATG-TGAATCTTAGGTTGT 200883
QY 2393 gggcccttaaaaggacagaagtgaacatacagacagctcggatlttgagacgtaccc 2452
DB 200882 GAGCTTTAAAAAAGAGAGAAATCTGCATTTGGAGACTCGAGATTTAAAGCAAGTACT 200823
QY 2453 tgcgcatctcccaactgatatgaagcaactccctcactatctcggtctcgaagggttt 2512
DB 200822 TGCTATAGTCCACCACTGAATTAAGCCCTTCCTTCAACTCACTGCTGAGAGAGTTT 200763
QY 2513 tgcctgcgcatctatctctatattctgtgtccctgacccggaggaagtgattaac 2572

[illegible][illegible]

OY	4714	atcaaatattcccatctgcgacacttaacaagaacggttgttactcgttgtgcaatgycag	4773
Db	198644	ATCAACATATTTCACATCGCACCTTAAACAAAAGCAATTGTATGGTTTGCCATGCAATGGCAGG	19858585
OY	4774	cgaagggcccatctgtcccccttcacctaagtggtccctcagtcaccagagcgtyggc	4833
Db	198584	CCAAGGCCCGCATTTGTGTCGCCCTTCCACTANTGTGTGTCCTGCATTGACCAGCAGCATAGGC	19852525
OY	4834	tgcattgtagctcttttcacagatcttacagcctgaggtlaataagtcatgccaactctc	4893
Db	198524	TGCATGATAGGCTCTTTTCCAGAGATTCTACACTCTAGATATAAGTATGATGCAAGTTCTC	19846545
OY	4834	tcctgta-----tcccctgygggtcagccccagaggccaaccagcctcgtctcc	4943
Db	198464	TCTGCTAATTCTGTGAAGTCCTCGACAGGTCACTCCCCGCAAGCCATCCAGCTTCATCTCC	19840505
OY	4944	caacctaaagticcattoctatgctctctccaccaagagsgaaactiaagatccttgga	5003
Db	198404	CACAACCTTAAGTTCACCTTCCTTAACACTTAGAACCTA--AGACTTACCATTTCTTAAGA	19834474
OY	5004	ccttaagagatgcgatagccttaaagaatttcaaagagctatacgaatgcagccctgt	5063
Db	198346	CCTGAAGAGATACAGTGGCTTAAGAATTTCAAGAGCTTATCATATGATGAGCCTTCT	19828585
OY	5064	tcatcccccaagcggatgtygtgtgttatgcttgytgygaaccttacttggcacctctgcgaa	5123
Db	198286	TCATCTCTTGAGCCGGATGTGTGTGTGATNTGTGTGTAAGACCTTACTGGGCACTGTGCCAA	19822222
OY	5124	taactgaggtgycacctaacttaagtcagtygtctatcccttcaacctgycattca	5183
Db	198226	TAACTAGATGTGGCAATTGTGTGTTTAGTCCATTGGCATCCCTTTCACACTGGCATTTCA	19816767
OY	5184	tcaaacagaaggaggaab-----aataagacatgttaaagcgagaga	5226
Db	198186	TCAACCAAGGAATAATAATAATAATAATAATAATAGGACATCTATAAGCAGGAGAA	19810707
OY	5227	gccccctataggtcttcgcacctcgcacgtccattitlagcgcgaatlvyagtlcccaag	5286
Db	198106	G--CCCTTATAGGCTTTGCACTCTGCACATCTATTITGATGCATTTAGACCCCGCAAG	19804949
OY	5287	aatcccaatcaatttiaagctltgaatcgaatgacacagccaaaatttaafgcataattta	5346
Db	198048	AATTCACGATTAATTTTAAGCTGAAATCAATAGTACAGAGATTTAAGTCAATATTTTA	19798989
OY	5347	gtgagtga-tgttaataaaaatgtlaaatagataatatctatatacacaacaagca	5405
Db	197988	GGAGATGACAGTCAATATAAATGTAGATTAGATAACTACATCTATTATCAACCAACAGCA	19792929
OY	5406	acaagctttcaatggt--gaaagaaaaactcaggtcgcgccagccctvgggctact	5463
Db	197928	ATGAGCTTTTACACAGTTAAAAAAAAACTCTTGTGCAGCACAGCCCTGAGGCTACTCT	19786969
OY	5464	gacctgcagaaagtgccacactctatgtgycaaaaaanaaaaaaaaaaaggccatct	5523
Db	197868	GACCTGACAAACGTTTACACTTATGTGTGCAAA-----	19783232
OY	5524	ataccaattcaagltlaatttagactaacaagaagcttctactcatagcaaaagataatga	5583
Db	197832	-----	19783232
OY	5584	aatcccaacttaagaagtttcaacaaaagtaagttgtctaanaagttaacagtytaac	5643
Db	197832	-----	19783232
OY	5644	atgatataagtaactctaaactcttgygccttagacagctagttccacagataaaga	5703
Db	197832	-----	19783232
OY	5704	aagttcacttaaaaaaaaaaaaaagaatggttatcttcaaaaaaaaaaaatgycagtt	5763
Db	197832	-----AGAAAAAAAAAATGGCGATT	19781313

QY	5764	ggaagtttaaccacagacgtgtgagctctgcgcgaagcgcaagggcctctctctaaaaaca	5623
Db	197812	AAAGTTTAACTCAACAGCTGTAGAGCCCTGGCCAAGGCCAGTGGCCAACTCTCAAAACAA	1977535
QY	5824	ctagaatgggttctccaaaggctggcccccacatctaaagggccctggcagcaagccctg	5883
Db	197752	CTAAGTTTG6GTTTCCAAAGGCTAGCCCCCACTGTCCTCAAAAGGCCCTAAGACATGGCCCTG	1976992
QY	5884	ttagcaacaagaagcagataaagctaaactcttagcgaaaaacctaaacataaagtcctcccca	5943
Db	197692	TTACCAACAAGAAGCGAGTAACTAACTCTTGTAGACAAAACCTAAACATTAAGATCGCCGCC	1976333
QY	5944	tgcgtgtgtgacttcaatcagttaccaaagsgacatctagc-----taat	5988
Db	197632	TCATAGCTAGTGGTGGATCTTTAATTAAGTAACTAAACGACTAACTATTACGTATAT	1975737
QY	5989	gaatgctagactaaactagatataccaaagcttctctgtgaaatcccccataaccattga	6048
Db	197572	GAAATCTTAGACTAACTAATATATACAAAGTTCTCTGTGGAAATGCCACAAACCATGA	1975133
QY	6049	aglttgcaacacccctaaaccccgccacccctgtccctggtaatcagagagccagtltaaca	6108
Db	197512	AGATTGCAACACCCCT--AACCCCGCACCTTACTCTCTAGTATCAAGAGCCAGTTAAACA	1974544
QY	6109	t-aactgtgtgaagtggtgtgacccagtttatcttaatggggcccaactccaaaacatc	6167
Db	197453	TAAACTGTGTGAATAATATTAGCTCATATTATTTATGTAGGGCCCAACCTCGAGACTAAC	1973944
QY	6168	cttaaacatcagtaaacctggagagctgtaagctggaatggagagcagcttaccacactcgca	6227
Db	197393	CTTTAAATAATCACTAGACTAGAGACTGTACATAGTATAGGAGACAGCTTGGCCAAACCCTGCA	1973334
QY	6228	aagtgactcagaaaaaag-----ccctgtctcagtcacacaccggaagctgactgtcc	6279
Db	197333	AMGTACTCTGAGAGAGACACAAACCCCTGCTCCAGTCACACCCAGAGAGCTGACTGGTCC	1972744
QY	6280	acgcagcgcgcgaagcagatagaanaacctcaatcagggactcatcttccctaaattggact	6339
Db	197273	ACACATATACCCAAAGAGTGAAGAACTATGTGCACACTCATTTTCCCTTAAATTTGGACT	1972144
QY	6340	tgtaaagaagaagactcaactgacacctccctcagactgaagactgtccaggtatatacat	6399
Db	197213	TGTAAAGTAAAGACTTCACTAGACCTTCTCTAGACTGAAGACGTGTTCACGATATATCAT	1971544
QY	6400	caagtcactggagttaggcaaaaagattgctcaaatccatatttcaatgttcaatgaag	6459
Db	197153	CAAGTCACTGAAAGTAAAGCAAAATATGCTACAGTCCCTATTATTATTATTTATTTGAGG	1970944
QY	6460	tgtacgagagactctaaagaaacttgttctgtataatgctatctcatcagaagtaatgac	6519
Db	197093	TGTACCAAGAGACTCTTAAAGAAACTTTGTTGTATATATGCTATTGTATCCAAAGTATGAGC	1970344
QY	6520	ctaggaataaaccaacctgatgtgtgttaagacccatttcaagcctccaatgatcaagct	6579
Db	197033	CCAAAGAAAT---AACCTGATGATCATGTTATATGACCCCAATTTAAAGCTTCCCATGATCAGCAT	1969784
QY	6580	tttttaaaataaataagactgtgtcttttctctgtaggaacagaagtaaaataatagctaa	6639
Db	196977	TTTTTAAATTAATAATTTAGAGCTGTGCTCTTTCTTAAAGTGACACAGTAAATTAATATAGCTAG	1969184
QY	6640	gacacagaagaagaggaatccccaagactgttaacactaaatctaatgtctgtgccat	6699
Db	196917	AACACAAATAAAGAGGGGTCCCAAAATATGTAACCTTAAATTTTGTCCTGTGTG--CGCTAT	1968599
QY	6700	caatgcaatcgcgcatagataaagatgcggttcttcaactgaaaaaataaagaatgaca	6759
Db	196858	TGATATGTAGACAGCATGTGAATTAATCATCTCAGTCTCTTAATTTAGAAAAAAGTTACACAG	1967999
QY	6760	cagcgagaaataagtatatactgcgcaggaataagactcaatgtgtgcaaatgtgtgtaattac	6819
Db	196768	TAAATAAAATAGTATATATCTGTGTCAACAAACATATTTATCT---AGATGTGTCAATTACT	1967422
QY	6830	ggtctctgtcatcatcaggtctacttagaaaaagatgtgaaaaagccctgttcttactccaa	6879

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Db 196741 AGCTGTGTCATTAGCTAGTCTGTAAGAAAAAATATAAAGATCCGTGTACTCCAAA 196682
QY 6880 aaggagaagcagccctcctctgtagagtggaagctgcgaaccccttgaaattgtaatta 6939
Db 196681 AAGGAAAGCAGCCCTCTCTGCAAGAGTAGAGCTGCAACTTTTAAATTCATATCA 196622
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Db 196384 TCATGTATGTTTGTAAATTAAGTGTATATAAAGATCAATGGCCATAGAGCCCAAGAA 196325
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QY 7299 tcttaggtctaaagtctcaattattagacaattatgtacatgctgaaaaagaaagaa 7358
Db 196264 TTCTAGGTTCTAAATTCATCAATTAATGTGACAAATATGTCAATCCAGAAAAAACA 196205
QY 7359 ttcaaccatccttagagtagtacttagttgcttaggacaanaactgtataatgttaccaca 7418
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QY 7419 aaaaacagttacatgtgtgagttcaaacacacagataaanaatcattcagtaattcca 7478
Db 196144 AAAACAGTTCATGTGTAAGTTCATTAACACAGAAAGAAATCCATTCATTAATTTCCA 196085
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Db 196084 AAGTTTCAG-CCGTAAAGTCCACAGAAATTCGA-CCGAGCATGGACAG-CCCCACACAG 196028
QY 7539 gctactcgtgatacgtggacatagaaactacgttaagctgctgacacatgtagacatga 7598
Db 196027 GTTATCTGATCTATAGACACAGAGCTTATGCTAAGCTACCTGATCAGTAGACAGGTAG 195968
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Db 195967 CTGTGTAATGGACACATTAAGCTGTCCATTTCTTCTGTGTCATATAAACAAGTGAA 195908
QY 7657 ctctctggtctctcgtctatgcttcccggaagcgaacatagccatagataatcaa 7716
Db 195907 TTCTCTAGGCTTCCAGCTCTATGCTTCCCATGAAATAATGAAGCATAGCATAGTGAATTAA 195848
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Db 195847 AAAGATTAATGAATGGCCCTGAAATAATCATATACATATAGACCTGTGCACTTTAGGCA 195788
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Db 195787 CAAGATGGCTCATTAAGATATTCAGACCCCATTTACAGGCTCAACCAATATCAAGGTTA 195728
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QY 7895 gcaagaactcagataagaatgtctatcaataatagatgtgctctcgactactt-ct 7953
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Db 195667 ATGAGGACTCTGATGAGAAATGCTGTCTATCAAAATAGACTAGCTCTTGACTTGTCT 195608
QY 7954 agcagctgaagaagatgcttata-aaatttaaccttacttaattactgtctacacataga 8012
Db 195607 AGCAGCTGAAGAGAGAGTGTGTAAGAAATTTAACTTACTAATTTGTTCTACACACAA 195548
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Db 195499 AGCATGTATCCCGTGCAGAGTGTGSCACAGACTCAATCCAGAGCCATTTTGAAGATTA 195440
QY 8133 gtcccaagcactagaagagattaaaccttat-ataaggatataatagtaataagaac 8191
Db 195439 ATT-CCAGAAATATAGAAAGATTTAAACTCTTTATTAATAGATATATATAGTAAGAGAAC 195381
QY 8192 ctgcttaactgtccctctgcttgcctgtacgtcttacttcaatgataaaaaagcttactgc 8251
Db 195380 CTGCTTACGCTCCCTCTGCTGTGATACCTGTATTTCCAAATGATMAAAACTTCCTGCC 195321
QY 8252 taacttagttccaaatgacctcaacacagctgtactatagaaactatcaatctat 8311
Db 195320 TACCTTAGTTACCAAAATACCTTACACACAGCATCTGTATTAATCACTATCAATCTAT 195261
QY 8312 tgcacaaagaagcatalaagtgccaaaaataagaagtgaacatccactaat-aaaaagtga 8370
Db 195260 TGCACAAAAGACATATAGTAGCAAAATATAGATGAGATGGAAGTCACTCCACTATATAAAGTGA 195201
QY 8371 ggtctcacaagggggaatagggggaagagaagacccctcatatgtttatattgtt 8430
Db 195200 GAGTCTCAAGAGAGGAAATGAGGGAAGAGAGACCCACTATATGTGTT--TATGTT 195143
QY 8431 ttaactcagaagaagacagagaagcgaactaaagcgcggtagcccgcgccaaagac 8490
Db 195142 TTATATCTAGTACCTCTTTTAAAGAAAAACAAGAGAG-----AA 195101
QY 8491 cagaccgaacccagcctggtgctctgacctgaagcctggttagttaaatcgaccc 8550
Db 195100 GTTAAAGACAGCAGCCCTGCGCTCTGCTTAACCTTAATTAATAAATCAACTCA 195041
QY 8551 tgaccatgaactgttgttatctatagatctcaacaatgtatgtaagaactgtgaa 8610
Db 195040 TAACTTAAAACTGATTTATTCGTAGATTCCAGATTTGTATAGAAAGCAATTTGAA 194981
QY 8611 tctctcgtctgtctgttcaactgtgacacacagctgctcaagcccgtaacgtacc 8670
Db 194980 CTCCCTGCTCTGTTCTTCTCTGACACCGGTGTCAGAGCCCTGTGATGTAACT 194921
QY 8671 cctggtctacatcgaatcgaacccctctcatgtgcagaccccttagagttgtgagcct 8730
Db 194920 CTTGATTGCTCAATATCATCAGACCTTTCAAG-TGAATCTTTAGTGTGAGACCTT 194862
QY 8731 taaagggcagaagttgagacaccttgacagctcggatlttagagcgtacgctcgcat 8790
Db 194861 TAAAAAGGACAGAAATTTGATTCAGAGAGCTTGATTTTAAACAGCAGCTTGCTGAT 194802
QY 8791 tctccagctgtgtaaagcaccctcctcaactatcctcgggtctgaggggtttctctc 8850
Db 194801 GCTCTTAGTGAATTAAGCC-CTTCTTTTACNACTGATGCTGAGAGTGTGTCTGT 194743
QY 8851 agctgctcgtctacactcagc 8874
Db 194742 GCGTTGTCTGTCTACACTGGAGC 194719

RESULT 4
HS4546 79376 bp DNA PRI 23-NOV-1999
LOCUS
DEFINITION Human DNA sequence from PAC 45466 on chromosome 1q24. Contains
transcription start site, 5' UTR, exon 1, intron 1, exon 2, intron 2, exon 3,
intron 3, exon 4, intron 4, exon 5, intron 5, exon 6, intron 6, exon 7, intron 7,
intron 8, exon 9, intron 9, exon 10, intron 10, exon 11, intron 11, exon 12,
intron 12, exon 13, intron 13, exon 14, intron 14, exon 15, intron 15, exon 16,
intron 16, exon 17, intron 17, exon 18, intron 18, exon 19, intron 19, exon 20,
intron 20, exon 21, intron 21, exon 22, intron 22, exon 23, intron 23, exon 24,
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ACCESSION 298750
 VERSION 298750.1 GI:2887277
 KEYWORDS 1q24; myocillin; TIGR.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eukarya; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 79376)
 Deadman, R.
 Direct Submission
 Submitted (27-OCT-1997) Chromosome 1 Project Group
 (http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk Clone requests: clonequest@sanger.ac.uk
 On Feb 14, 1998 this sequence version replaced gi:2465060.
 IMPORTANT: This sequence is not the entire insert of clone 454G6.
 It may be shorter because we only sequence overlapping sections
 once, or longer because we arrange for a small overlap between
 neighbouring submissions.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variations annotated may not be found in the sequence submission
 corresponding to the overlapping clone as we submit sequences with
 only a small overlap as described above.
 This sequence was generated from part of bacterial clone contigs of
 human chromosome 1, constructed by the Sanger Centre chromosome 1
 mapping group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr1/
 This sequence has been finished according to sequence map criteria
 as follows. An attempt is made to resolve all sequencing problems,
 such as compressions and repeats, but not necessarily within known
 annotated human repeat sequence elements (e.g. Alu). Where the
 sequence is ambiguous, there is an annotation using the 'unsure'
 feature key.
 The true left end of clone 454G6 is at 1 in this sequence. The true
 left end of clone 560B9 is at 79273.
 454G6 is from the library RPC13 constructed at the Roswell Park
 Cancer Institute by the group of Pletzer de Jong.
 For further details see http://bacpac.med.buffalo.edu/
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 AA313383; match: AA163561 F02925 AA131540 W00634 R36066;
 match: AA313383 AA163561 N89173 AA174814 AA057059; match:
 AA329084 W437082 AA043955 AA341783 AA333681; match:
 AA046487 AA369741 H08313 AA186895 H32730; match: H08333
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Query Match      14.0%: Score 3494; DB 11; Length 79376;
Best Local Similarity 76.5%: Pred. No. 0;
Matches 5300; Conservative 0; Mismatches 970; Indels 654; Gaps 57;

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DB 11727 AGGGTGTGCTGATGTGGAC----- 11748
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QY 2922 actggtcttggaacttgcacactccatcccactcattgagtgaaagcatgagcctga 2981
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 11748 ----- 11748
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2982 tctgatacccaagtggtgctgtctccgcaacttggtttgttttgactgacttag 3041
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 11748 -----TTTGTCTGTGGTTTGACTTGACTTGA 11774
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 3042 atgctgataacttggtttggtttltgacctgctgtaattctcgaatactcgtatctt 3101
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 11775 ATTGCTGACACTTTGGTTTGTAGTTTGACTTGGCTGAATTTTGTGTAACAGGATTTT 11834
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 3102 ggtt---tgatttggtttagtgtaactgcgaagaagtgtgctgctgttaccgcg 3158
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 11835 GAATTTGCTATTTTGGTTTGTATTAACAGTAAGATGTGGGTGTGGCCCTTTACCCG 11894
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 3159 ttctctgttggtggtgtgactg--gtgtgagagtggtgttcttcgaag-----a 3211
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 11895 TTCTTTGTCTTGTTGTGAGTGTGTGTGTGTGACGTGTGATTTTGTCTCAAAAAA 11954
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 3212 aaatggttcaagcaca--taagccacactactagaacatatgttgaaaaaaattcaag 3270
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 11955 AAAATAGTCAAGTGCACAAAGTAAGCCACCCACTGGAGACTGTATTAAGAAATTTCAAG 12014
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 3271 aaaggaattaaaggagagatcgggtgttactatgaacactagaacacttagaacttgt 3330
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 12015 AAAAGATTTTAAAGGAGACTGTGAGATCATTACCTCCAGAAACCTTAGAGATTTGTGT 12074
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 3331 aaataagactgycacaactatagagtggtgtggtcactcaagaagaagccctagaaggtcc 3390
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 12075 GACTTAGACTGGCCAGCATTAAGAGTGTGGTGGCCATCAGAAAGAACCTTAGAGGTCC 12134
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

OY	3391	cttttccaattgtatggcacaaagttaacccgttaagccaaagcacagacagatcttg	3450
Db	12135	TTTGTTTCAAAAGTATGACACAAAGTTAACTGTAAAGCCAGACCCAGACCAATTTCG	12194
OY	3451	tacgtagaacaattacagcttgglttttagaccccttcgccccacagtagttaagagagc	3510
Db	12195	TACATAGACACTTACAGCTGTTTTAGAGCCCTTCCTCCGACAGTGGTTAAGA----	12250
OY	3511	agaaagagaggaagaacaagaggc aaagaaagaaagtc aaagagagagagagagag	3570
Db	12250	-----GAAACACACATRAAGCGCTGCGACAGGCMA	12280
OY	3571	agacagaaagtc aaagagagaagaanaaaatagagagaata tccaagtagttaagaaaa	3630
Db	12281	GGAAGACACACAGAGAAAAGAGACCAATCTATACAAATCTTAAGTTAATTTAGACTA	12340
OY	3631	aatgtgtacacctttccctttaaagccaaagtgtaattttaaaccttaaatltgtaatt	3690
Db	12341	AACAHG--CTTTAATATAGCAAAAAGATATGTAAATCCCAACTTCAAGGTTTCA	12398
OY	3691	aaaggtatccgcgtlaaccctgtlaacacatctaataccaccttgcgtgttagtgaacaag	3750
Db	12399	CAAGTGAAGTTTGCTAAAGTTACACTGTATACACTGTATATGTATGTACTTAACTCTG	12458
OY	3751	ggcgtatccgaaagcaactgaggcccttcatacaaaaaccttaaccagtaaccacag	3810
Db	12459	-----TAGCCTTAGACAGTGTAGTCCAAACATTAAGAAAGT-----	12497
OY	3811	atggccacagatgcattcaatctgttagcagcagctccttgcatacaga aaaaaaaa	3870
Db	12497	-----TGCTTTAAAAAAGAAAGAAAGATGTATCTTCA----AAATATAAG	12543
OY	3871	aaagagctgttgggaaggcaaaatttagtlaaaagaagtgtatagtbaatctctgctc	3930
Db	12544	AAAAAAGGGGGGCGGCGACAGATTATGT--AAAGAGGTATATATGTAAATTTCTTCTC	12601
OY	3931	tgaataaatttaactgt-ttgtttaaagaagaataatttgttaataagtcagaaagttag	3989
Db	12602	TGAATTAATTAATCTGCTGTTGTTTAAAGAAAAAAATCTTGTATATAGTCAGAAAGTTAG	12661
OY	3990	acatgtc aaagaattatctgcgaagtcataagaaacagatltata-aaaaattatgca	4048
Db	12662	ACATGTTGAAAAATTTGTGCGAAGTGTGTAAGAAAAAATGTATATAAAATATATCA	12721
OY	4049	aaaaaatctgtataatttgaagaagtaataagcccttcgaagtaac- atgaaagaacagt	4107
Db	12722	AAAAATGTTGATATATTTAAAAAGTATTAAGCCCTCTCAGTACGTTTAAAAAACATTT	12781
OY	4108	tatgtc aaagtgatcaagaagaatlaaataatactcttggttaaaagaatgtgaagagagc	4167
Db	12782	TATGTGCAAACTGTATAGAAAAGTAAAAATGCTTATAGTAAAAAGTTTAAAGGGGC	12841
OY	4168	ataagaatlyggaattttaccatacaataaagytlaaaaaaatatgttttgaagttt	4227
Db	12842	ATTAAGAACTGATTTTACTACTATTAAGGTTAAAGAAATATTTGTTT-----	12893
OY	4228	aagcaagttttaaanaatgttaatttgaaaaaaaatctcgtgtgttaactaatttgctaa	4287
Db	12893	--AAAAGTTTTAAAAAGTTAAATTTGt- AAAGAAATTTCTGTGTAAACATTTATGCTTAA	12949
OY	4288	gataaaagagatcatccagttctcgttgacgtggaatcaaaagtaaaatgtgcaacag	4347
Db	12950	GTTAAAAAGTATCATCCAAATTTTTCGTGTAACATTAAGTAAATTAAGTAAATTCGACACGG	13009
OY	4348	ttttcttgaagcacaacactgtctttaa caaaaatataaaagytlaaaagaagcttg	4407
Db	13010	TTTTTCTTAAAGCATCAACCTGCTCTTTAAACAAAATATATAAAGTTAAAAAGTGTCTA	13069
OY	4408	taaaaacttaccattatgttcaaaacttgaaaatgtgataaaatagtctatgtaggtttat	4467
Db	13070	TAAATCTTACCTTATGCTCAACCACTAAAAATTAAGTAAATATATGTCTCAAGAGGTTTAT	13129

QY	4468	taaatatgaatttaacatttaacacacataataaagaatnaattagcttctcgtt	4537
Db	13130	TAAATTAAGATTTAACATTTAATACACCCTTAATATPAAAGTAAATTTAACTTAGTACGTG	13138
QY	4528	ataaaatcacagaagatattataataataaattggtgtttagcttctctgtccta	4587
Db	13190	ATAAAAATCATACAGACGATTAATTAATTAATAATAGTGTTAACCTTCTTTGGTCTA	13244
QY	4588	aaaactaat-aaaaatagcctcctaaagaaacattcatttacttgagatcatagaagt	4646
Db	13250	AAAACTATATAAAAAATAGATGCTTAAGAAAGAAACATTCATTTATCTAGAGATCATAGAAGT	13350
QY	4647	taagaacttaaaacaacatttggcaattaaagaacatcaccaatggcaatgtccgtgtt	4706
Db	13310	TAAAGACTTAAACAAACCTTGGCATTTAAGACGGCATACCAAGATGCAATAGCTGGTT	13356
QY	4707	gaattgcatcaaatatcattcattcgtcacattaaacaagaacagttgttatgtctgtgaca	4766
Db	13370	GAATTAAGATCAAAATATTCCATCTGCACGTTATA-AAAAGCAATTGTATGCTTGGTGCACA	1342
QY	4767	tgggaagccagaagggccctatttgtccccccttcactaaagtggtctctcactcaccaagg	4826
Db	13429	TGGAGGCCAGAGGCCCGCGATTGTCCCGCTTCACCTAAGTGTGCTCTCCAGTCCACCAAG	1348
QY	4827	cgttgagctgcatgtgtagctctttccaggattctcaagccttgaatgaatagtcagca	4886
Db	13489	CGTGGCTGCATGTGAGCTCTTTTCCAGATTCCTACAGCTAGACTAGATTAATAGTCATGCA	1354
QY	4887	aactctctctgcta-----tcccttgygttcagcccccagggcatalcaagctc	4936
Db	13549	AGCTCTCTGCTATATCCGAGTCCCTGCAGGTACGCCCAAGGCCATCCAGCTTC	1360
QY	4937	cgcttcccaactaagtttacttctatgtctctcacacagaaggaac---ttagat	4993
Db	13609	CGTGTCCCAACACTAAGTTACTCTGTCCTCTCATGCGAGGAGACACTTATTAGAT	1366
QY	4994	tccttgaagaccgaagtgatgtaagaatgacctaagaatttcaagagcttcaatcagt	5053
Db	13669	TCTTTAAGACCTGAAAGGATGAGTAGACCTTAAGATTT-----TCAACCACT	1371
QY	5054	cagcccttgttcataccccaagcggatgtgtgtgttatgttgytagaccttactgagca	5113
Db	13718	CAGCCCTGTTTCCCTCCCGCAGCAAAATGTGTGGTATCTGTGATGACCTTTACGGGCA	1377
QY	5114	ctctgcgcaataacttggagtgtgcaattactttgtccagtgtgtatccctttcaacc	5173
Db	13778	CTCTGCGCGATTAACCTAGAGTGGACACTTGTGCTTTAGTGCACATGGCTATCCCTTTCACCC	1383
QY	5174	tgtgatttctcaacaagaagg---ggggaaaaataagaatcgttaaaacggagaaagccc	5230
Db	13838	TGGGATTTCATCAACCAAGAGAAAAACAAAATAATAGACATCGTAAATGTAGAGAAAG--C	1389
QY	5231	ccttataggcttctgacatccacgtccatctttagacgcaatttgaagtcaccagggata	5290
Db	13896	CCTTATAGTCTTCAACTCTGCACATCTTTAAGTGCATTTGGAGCCGCCAAGAATA	1395
QY	5291	ccagatcaattaaagcttgaatacaaalagctacaanaattgaatcaatatttagtga	5350
Db	13956	-CAGATCAATTTAAAGCTTGAATCAAAATAGTTTACAGATTTAAATCAATTTTATAGAG	1401
QY	5351	gttga-tgttaataaaatgttaatatagataattatctattacaacaacagcaaca	5409
Db	14015	ATGCACTCATATAAATGTAAATTTGATTAATCTACATCTATTACCAACCAACACCAATGA	1407
QY	5410	gctttcataagtt- gaagaanaaactcaggtcggcccccagcccttggggctacttgacct	5468
Db	14075	GCTTTATATAGTTAAAGAAAGAAATCTATGTGCGCCCCCGCATAGAGGCTTACCTGACTT	1413
QY	5469	gacgaagtcacacatctatgttgcataaaaaaanaaaaaaaggccatctatacc	5528
Db	14135	GAATAAACTGTTTACACTCTATGTGTCAAAAAGAG-----	1417
QY	5529	aattctaaagtaatttagactaacaaggcttactcatagcaagaataattgaatcc	5588

Db	14170	-----	14170
Qy	5589	caactttaaaagtttccacaaaagtaaagtttgtaaaagttaacagtytaactgta	5648
Db	14170	-----	14170
Qy	5649	ttatagtaactctaactcttgygccttagaagtcctagtcacagataaagaagtt	5708
Db	14170	-----	14170
Qy	5709	cacttaaaaaaaaaaaaaagaatcgttatcttcaaaaaaaaaaaatgcagttgagtt	5768
Db	14170	-----	14188
Qy	5769	tttaaccacagctctgaagctctctgcacaggccagtgccctctctcaaaacactga	5828
Db	14189	ttttaaccccgactgtaaggcccttgcccaaggccagtgcccttctctcaaaacactga	14248
Qy	5829	tggggtttccaaaggctggcccccatatctaaggccctcgagaaaggccctttagc	5888
Db	14249	cagcgtttccaaaggctggcccccatatctaaggccctcgagaaaggccctttagc	14308
Qy	5889	acaaagaagcagaataagctaacctcttaaggcaaaacctaaacataaagtcccccctgctg	5948
Db	14309	acaaagaagcagaataagctaacctcttaaggcaaaacctaaacataaagtcccccctgctg	14367
Qy	5949	tgttgactttaactggtaccagaagacatcatatgataatgatactgacaaactaat	6008
Db	14368	tgttgactttaactggtaccagaagacatcatatgataatgatactgacaaactaat	14427
Qy	6009	accaaagctctgctctgtgtaaaatcccccataacatcattgaagtgttgcaacacctaaac	6068
Db	14428	accaaagctctgctctgtgtaaaatcccccataacatcattgaagtgttgcaacacct	14486
Qy	6069	ccgcaacctctcctctgtaatacagaagcccaagttaaacat-aactcgtgtaagtgctg	6127
Db	14487	ccgcaacctctcctctgtaatacagaagcccaagttaaacat-aactcgtgtaagtgctg	14546
Qy	6128	gactcagttattcttagtgggcccacacccccaacacatcccttaaacatcagtaaacctg	6187
Db	14547	gactcagttattcttagtgggcccacacccccaacacatcccttaaacatcagtaaacctg	14606
Qy	6188	gagctgtacgttgatgagagcagcttccacaaacctctgcaagtgactcaga-----	6240
Db	14607	gagctgtacgttgatgagagcagcttccacaaacctctgcaagtgactcaga-----	14666
Qy	6240	aaaagccctgctccagtcacacccgggaagctgactcgtgtccacgcacgycggaagctag	6299
Db	14667	aaaagccctgctccagtcacacccgggaagctgactcgtgtccacgcacgycggaagctag	14726
Qy	6300	aaaacatcacagggaactaatcttctctaaatttgagactgttaagtaaggaacttcagc	6359
Db	14727	aaaacatcacagggaactaatcttctctaaatttgagactgttaagtaaggaacttcagc	14786
Qy	6360	tgaccttccacagactgagaactggtccacagataatacaagtcactgtagtagaca	6419
Db	14787	tgaccttccacagactgagaactggtccacagataatacaagtcactgtagtagaca	14846
Qy	6420	aaaagatgctacagtcactatatttcaatggttattataagtgtagcaggaactctaaaga	6479
Db	14847	aaaagatgctacagtcactatatttcaatggttattataagtgtagcaggaactctaaaga	14906
Qy	6480	aaactgttgataatgctatctatcaataagtaatgtagccctaggaataatacaacctga	6539
Db	14907	aaactgttgataatgctatctatcaataagtaatgtagccctaggaataatacaacctga	14966
Qy	6540	tgtgtgtaatacgaactttaagccctccacatgatacaagtttttcaaaataactaaaga	6599
Db	14967	tgtgtgtaatacgaactttaagccctccacatgatacaagtttttcaaaataactaaaga	15025
Qy	6600	ctggtcctttcttagtgacacaagtaaatagcttaagacaagaagaagaggtatcc	6659

Db	15026	CTGTCATCTTCGTAAAGTGCACACAACTAAAGTATATGCTATGAAACACAGACAGAAAGGCTCC	15085
QY	6660	ccaagcagtgtaacacctaataatttaagtctgtgtccacatacatagcaatcgycataagaa	6719
Db	15086	CCAAAAATGTACCTTAAATATTGACGGCTGTGCCACTATTAAATATATAACGACATAGA	15145
QY	6720	taagatgcggtctctttaaacttgaataaaaaaaagttcacacgaggaataagatatac	6779
Db	15146	TGAGATGCGGTTCTCTTA-----GATTAGAAACAAAGTTACACGCGAAATATGATCATATC	15201
QY	6780	tcccacgaattagctcatctgtgcaaatgtgtttaactgtgtctgtgtcatctagact	6839
Db	15202	TCTCAAGATCTATATTATGT---AAGATGTCTCAATACTAGTCTTGTGTCTTTAGGCT	15288
QY	6840	acttgaataaaagatctgaataaaagaccctgtttagctccaaaaagagaagcagcccttc	6899
Db	15259	ACTTTAAAAAGAAAGATATAAAAAAGATCCTGTGTTAGTCTCAAAAAAGAAAGGCGCCCTCC	15318
QY	6900	tgtacagatgtgaagctgtcaaccccttgaaattagtaattacaattccctttaaaccgaag	6959
Db	15319	TGCACGAGGTGAAGGTGGCAACCTTTAGATTATGTAATCACAAACCCCTCACAACCCAAA	15378
QY	6960	tagaataaaagaagtcacacgttactctctggcgtgcataaaaaagagctagatccagaat	7019
Db	15379	T-GAATATAAGAAAAATACGTATCTATTAGGCACTTATGATGAAAAAGGACATAAGATCTTAGCAT	15437
QY	7020	aaataccttagtaaaagaaggaggtctgttaactctctccgaaacagtaattcaagctt	7079
Db	15438	AAACATCTCTAATAAAAAGAAAGATTCAAAAGATGCTCTCCAGAACAGATTTTCAACACTTT	15497
QY	7080	ctataattacctaattgtgcgcagctccagagctccaggaataaccaga-aattgcttt	7138
Db	15498	CGTGATGTAGACTAAATATGTCCGATGCTGAGATTCACGAAAAACTAATTTTTTTTTTT	15557
QY	7139	tgcacattagccagacatgtagccagctctctaaatgtcaaccctcagttacglttgag	7198
Db	15558	TGCATTAGCCAGCATGTAGGCCCAAGTCTCTAAATGTCACTTCACTTACGTTTGGAAG	15617
QY	7199	aaactgtataaagatacaatgtgcataaagcccgaagaattagtgcctacagaccagt	7258
Db	15618	AAACGTGTAGTAAAGATCAATATGCGATTAAGAACCCGAGATTAAGTGCCTACAGACCCAGT	15677
QY	7259	tccigtatgaattcccgccgcaaaaagaatcacacctataattctcgtgttctaagaagctc	7318
Db	15678	TCCCTATGATTTCCCGGCCCAAAATAATCACCTCATATTTCTGTGTTCTAAAGCTTC	15737
QY	7319	aatttttagacatactgcatagtcgtgaaaaagaaagaattcacctacatccctgtagagt	7378
Db	15738	AATTATTAGACATAATTTCATATGCTAGTGAAGAAAGAAAGAAATTCACATCTCTGTAGGATG	15797
QY	7379	acttagtgccttaggacaaaaactgta-taatgtacac-----	7418
Db	15798	ACTTATGTCCTAAGACAAAAACCAATATTATTAATAGTACACACACACACACACACAA	15857
QY	7418	-----aaaaacagttaacatggtgtgagttcaaacacacacagataaaatccaattcaagtaa	7471
Db	15858	AAAAAAAACAAACATGATGATTAAGTATCCAGTTACACAGAAAGATATCCATTACATGA	15917
QY	7472	atttccaaagtgtgcagacggttttaagcccaaccacaaatctccacgggacgtacagcccc	7531
Db	15918	ATTTCCAAAGTTGCAGACTGTTTATGAGCCCAACCAATAATCCACACAGGACTGAGC-GGGCC	15976
QY	7532	ccaactagcctaacgtgatagttgagacataagacatacgttaagctgtgcacagtgta	7591
Db	15977	CCACACAGGTATATTGGATATTTAACACAGAGCTTCTGCTTAAGCTGCTATATCATGTGA	16036
QY	7592	caggtagttgtgtatctggcaactataaacatcttcttcctactgcccatacaaatag	7651
Db	16037	CAGGTAGCTGGCTAATT-GACACATTAAAGCATCTTTCTTTACTGGCCATA-AATCAG	16094
QY	7652	gcgaaccctccgggtctccctgtctatgctttccgcgaagaagcgaaacatagccatagata	7711
Db	16095	GTGAACCTCTAGGGCTCCACAGCTCTATGCTTCCCGGGGAAACGAAGCATATGACATATAGA	16154

Oy	7712	atcaaaagatgataatgaccact-----aaaaatatcaatactataaggctgc	7765
Db	16155	ATTGAAAGATGACCAATGACCTCCTTAAAAAAAATTATACATATCTATAAGCCTGC	162144
Oy	7766	cacttaagcaaaagttgctcctcgtgtatcacagcccccattcatgctcaactgaat	7825
Db	16215	CACTTAGGCACAGATGGCTCTAAGAGATGGAACCCCACTTCATGCTCAACCGAAT	16274
Oy	7826	catagctgtcgaagctgtttttagaatcatcactaataaaccaagctcaagccttgactat	7885
Db	16275	CATAGGTTACAGCTGTTTTAAATAATTATCTATAATAAACGGGTCAAGCCTTGACTGT	163348
Oy	7886	tctgcccgcgcaagaactcagataagaatgctatctatacaaatagatgtgcttcga	7945
Db	16335	TCTTCCCGCGCAAGACTCTTGAAGAGAATCTATCTATCAAAATAGACCGACTTGA	163944
Oy	7946	ctactt-ctagcagcttgaaagaggtctataaaatttaaccttactaattacgtcta	8004
Db	16395	CTACTTGGTAGAGGTG-----AATTTAACTTCATTAATGTGTCTCA	16437
Oy	8005	cacatagaataatcaaggcaagtagttaagaagttaaagacatagttaaaacatg	8064
Db	16438	AACATTAATATCAAGGCAA-----GTAGTTAAAGACATAGTTAAAAATAG	16485
Oy	8065	acaaaactgcaacatalgcccgtacgaglytgacaggaatcgaccctgaagccatgltt	8124
Db	16486	ACAAATAGACACATAGTCCCTTAAGGTAGCAGCGATGTGACCTTGAACCATGTTT	16545
Oy	8125	agaaggtgttccccgcacttgaggaatttaaactcttat-atagggttataagta	8183
Db	16546	AAAAGGTATTTCCCGCACTAAGAGATTTAAACTTTATATAGGAATTAATAGTA	16605
Oy	8184	atagaacactgcttaactcctccctgtgctgtgcctgtactcttcoaaatgtat-aaaag	8242
Db	16606	ATAGAACTCGTGTACTGCTCCTCCTTGTTGGCTACTGTACTCTTAAATGATAAAAAG	16665
Oy	8243	ctcatgtcaacttaigtaccacaaatgctcacaacaaglytactatagaatcacta	8302
Db	16666	CTTCATCCGTCATCTTAGTTCACCAAAATGCTTCACACAAAGTACTATATATAACTCA	16725
Oy	8303	tcaactcttgcagaagaagatagatgagcgaataaagatgaggaactccactaata	8362
Db	16726	TCAAACTATGACAAAAAGATATAGTAGCAAAATTAATAATGAGAACTCCACTAATA	16785
Oy	8363	aaaagtgaagatctcaaacggyggaatgaggaagagagaaacccctcatalgtgtt	8422
Db	16786	AAAAGTAGAGTCTCAAAAAGGAGAAATGAGGAAAGAGAAACCTTCATATATGTTT	16845
Oy	8423	atatgttttatatactcagaaaaagacagagaagcgaaactaaagcgagtagccgcgc	8482
Db	16846	ATACTCACTACTGTTTAAAGAAAAAGAAAAAACAAGAGAAATTAACCAAGACA	16905
Oy	8483	ctaagaacacagaccggaacacagcgcctggcctgctcctacctaagcctgtagttaaat	8542
Db	16906	GGCAGCCCGGCACAGCGCCCAAGGCTT-GGCTGGCTGGCCTTAATACCAAGTAGTAAAAA	16964
Oy	8543	tgcacccctgaactgaacaaatgtgttatctatagattccacacatgfatgaaagaca	8602
Db	16965	TCAACTCCTGACTTGAAATCCGATGTTACCCACAGATTTCAAGCAATTGATTAAGAACAA	17024
Oy	8603	tttgaagaatctcgttgtgtgtcttcttcaactgtagcaacaggtgtcagagccctgtc	8662
Db	17025	TTGTGAAGTCCCTGCTCTGTCTTTCTATTTCTACTACAGTGCACAGAAACCCCTGTC	17084
Oy	8663	acgtacccccctgcttactcaatcgatcacgaacccctcatatcagaccctttagatly	8722
Db	17085	ACTTATGCCCTTAGATTGGTCAATCAATCAACGACCTTTTCATG-TGAATATCTCAAGGTG	17143
Oy	8723	tgaagcccttaaaaggcagaagtgtgacaccccttgacgaagctcggatattgagacgtacg	8782
Db	17144	TAAAGCCCTTAAAAAGACAGAAATTTGTGCACTCGAGGAGCTCGAGATTTTAAAGCATAGC	17203

OY	8783	ctgcgcatcccccagcgcgtataaacgccaccacccctcacctctcggcgctcggagggtt	8842
Dn	17204	TTGCCAAATGGTCOCACGCTGATTAAGCC-CTTCTTTACAACTCGGTGTCTCAGAAGTT	17262
OY	8843	ttgtctgcagcttggtcctctcac	8866
Dn	17263	TTCTCTGGCGCTTGTCCTGTACA	17286

RESULT	5		
AF058907	DNA	PRI	29-OCT-1998
LOCUS	AF058907	Homo sapiens pleiotrophin (PTN) gene, exons UV3, UV2 and UV1.	
DEFINITION	AF058907 U71455		
ACCESSION	AF058907.1	GI:3790543	
VERSION			
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
AUTHORS	Eutheria; Primates; Catarrhini; Homnidae; Homo.		
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JOURNAL	PROC. NATL. ACADEM. SCI. U.S.A.		
MEDLINE	97121462		
REFERENCE	2 (bases 1 to 7728) Schulte,A.M. and Wellstein,A. Structure and phylogenetic analysis of an endogenous retrovirus inserted into the human growth factor gene pleiotrophin		
AUTHORS	J Virol. 72 (7), 6065-6072 (1998)		
TITLE	3 (bases 1 to 7728) Schulte,A.M. and Wellstein,A. Direct Submission Submitted (10-APR-1998) Pharmacology, Georgetown University Medical Center, 3970 Reservoir Road, Washington, D.C. 20007, USA On Oct 27, 1998 this sequence version replaced gi:1778411.		
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Db	56874	TTTTGTTTGTTCATCTTGACCCAGGGGGGTTCAAGCCCCCTTATCACGTACC	56933
OY	2340	cctggcttaactcaatcatgaacagacctctctatgcagaccctctagaattgtgaagccct	2399
Db	56934	CCTGGCTTGCTCATGTGAATCAGAGACTTCTCAAGTGTGACCCCCTTAGATTGTATCCCT	56993
OY	2400	taaaaaggagcagaagtltgagcalcaagagactcggaaattttlgagacyctagccctgcgat	2459
Db	56994	TAAAGGGGCACAAGATTGTAGCACCTGACAGCGATCAATTTTAAGACGCTAAGCGCTTTGAT	57053
OY	2460	tctccagctgtttaaagcacctcccttaactatctcsgtlgtctgaggggttttgtctgc	2519
Db	57054	GCTCCAGCTGATTAAGCCACTCCCTTACATATCTGGATGTC-----TCTGTGCC	57106
OY	2520	ggctaatcctgtatacttcttctgttctccctgcagcgggaagcaggtgatatacagatgtg	2579
Db	57107	GGCTGCTCTCTACTATTCTTGTTGTTCCCTGACCGGCAAGCGAGTGAATAAGACGCT	57166
OY	2580	cgaggcagctctctaaggcggctttagcctgtgccctgtgaaacalccctgtctggygactcca	2639
Db	57167	CCAGCAGAGCTTTAAAGCGGGCTTTAGCCCTGACCTGTGAAACATCCCTCGGGGAGACTCCA	57228
OY	2640	accagccagagtgtgaegcggaatcctctgaagaactctccgggtlaagcattgccccggtggga	2699
Db	57227	ACCAGCCGGAGGAGCGCGGATCTCTGAGACGGCTCCGGGTAGGCAATTTGCCCGGTGGGA	57286
OY	2700	caactccagagcagtggtgtgtgcagcccccggttgaggaatcaaaagtgagctgaacac	2759
Db	57287	TGCCTGCGCAGAAGCCGTGTGTGGCAGGCCCCCGTGAAGATCACCAAGTGGCTGAACAC	57344
OY	2760	cgggaagagaa-----ltgagcactgtgagctcggaacaaactaaacttlytlaagactagt	2812
Db	57347	CGGGAAGAGAACGTGGCACTTGGCACTTGAGTCCGGACGTCCTAACTCGSTAAAGACTAGT	57406
OY	2813	ctttggaactgtcccactccattltagavgaagcalgtgcctgataccaccaagcgctgacct	2872
Db	57407	CTTTGGAACTTCCACACT--CAATTGTAGTGAAGCGGTGGCCTGATCACCCACTTTGTGGCT	57465
OY	2873	ttataagac-----tfgtittgttttagtactgtgtttagattacttgacagagacgt	2925
Db	57466	TTATGGGCTCTTGTGTTTGTGTTTGTGATCTGTTGATTCGTTGAAGAGGATTG	57522
OY	2926	gftctvgggaacttgcaccatccatcccaactcaatctttagtvtgaaagcalgtgcctgtacgt	2985
Db	57526	AATCTTGGGAACCTGGCTACTCATTC-----GAGTGAAGACATGAC-----CTG	57566
OY	2986	alcaccccaagtgctcgtgttcccggaacttggttttgtttttagacttgaacttgaatgt	3045
Db	57570	ATCACCCCAATGATGCGCTGATACGGCACTTGTGTTTGTGTTTGTGACTTGACTTAGATG	57622
OY	3046	cttgaactcttggtttggtttttgaacgtgtcttggattctctaactctgatattttgtt	3105
Db	57630	CTTGATACTTGGTTTGTGTTTGTGACCTUGCTTGGATTTCTGATNCTCGAATTTGTGTT	57689
OY	3106	ttgattttgttttagttaaactctgaaaaagtgtgtgcgtcccttttagaccgttctttg	3165
Db	57690	TTGATTTCTGTGTGTGTTAACTGTTAAAGTGTGTGTGTGCCCCCTTTTACCCGTTCTTGG	57748
OY	3166	ttttgtgtgtgtcatgtgtgtgtgagagtgtgttltgtctcgaagaacaatgtgttcagcg	3225
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OY	3226	acaaa-taagcccaacctctatgaactatgtttgaaaaatttcaagaaaaagattttaagg	3284
Db	57810	AAAACTAAGCCACCACCCTCTAGGAACATGTGTGAAAATTTTCAAAAAAATTTAAGG	57865
OY	3285	agattacggtgttactatgaactatgaanaaacttgaacttbtgtttaaataagactggcc	3344
Db	57870	AGATTACGCTGTACTATATATACACAGGAACAACTTGAACATTGTGTGTGAATATAGACTGGCC	57922
OY	3345	aacattagaagtggtgtgtgcacatcagaagaagccttagacaggttccctgtttcaaagt	3404

D	57930	ACCATTTGAGTGGGTTGGCCATTGAGAAGAGCTAGACAGTCCCTGTTTCAGAGGT	57988
Q	3405	atgacacaagtgtaacctgtaagccaagcacacagaccagttctgtacgtagaacatta	3464
D	57990	ATGCACAAGGTAACTGTAAACCAAGGACCCAGACACAGTCGTTCCGTACATGACAGTTA	58049
Q	3465	cagctcggttttagacccctctgcgccccacagtaagtaag	3505
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Q	3505	-----agagcaaaagagagaa	3523
D	58110	TGGCAGAGGCAAGAAAGCCAGCAGAGAGAAAGAGAGAAAGAGAGAAAGAGCGCA	58165
Q	3524	gaacacagagggcaaaagaaagtcacaagagagagag	3559
D	58170	AAGAGAGAGGAAAGACACAGAGAAAGACAGAGACAAAGAGAGTCAAGAAAGA	58222
Q	3559	-----agg	3561
D	58230	GAGAGAGACAGAGAAAGATAGAGCGCAAGAAAGAGAGAAAGACAAAGCCMAAGGAAT	58289
Q	3562	gagagagagagacagaaagtcacaagagagaaagaaataagagagaaatcccaagtagt	3621
D	58290	CAGAGAGAGACAGAAAGTCAAGAGAGAAAGAACAGAGAGAAATATCAAGTAGT	58349
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D	58469	GTAACCAAGGGGTATCCGGAAGCAGCAGAGGCTTCCTATAGAAACCTTAACCCAT	58528
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D	58529	AACCTCGCGATGCCCAAGTGTGTTCAATCTTAGCGGACGCTTGCTTCTAACAGAA	58588
Q	3862	aaaaaataaaagagctg-----	3880
D	58589	AAAAAATAAAAGGCCATCTATACAAATCTAAGTTAATTAGCTAAACAGCT	58648
Q	3880	-----	3880
D	58649	CTTATTATAGCAAGAAATATTTGAATCCCAAACTACMAAGTTTCAACAAAGTAA	58708
Q	3880	-----	3880
D	58709	ATTTCCTAAAGTTAACAGTGTACATGTATTATAGTAACTTTAGGCCCTTCA	58768
Q	3880	-----	3880
D	58769	TCTACTCCACACATTAAGAAGTCCGCTTTAAAAAATAAAACAGATGCTATCTT	58828
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D	58949	CAGAAAGTTGAACATGTGCAAGAAATTTGCTCGAAAGTCGTGGAAGAAAAAGTTATA	59009
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Db	62521	AGGAAGAAGAGAGAGAACAAAGCCAGGTAGCCCGACGACCTGGAGAACCGACTGAAAC	62580
QY	8486	-----ccgaaccacgagccttgaggccctcgtacctaagccctgtaattaaatt	8543
Db	62581	AAGGAACAGATCTGAAACACGAGCCTGGGCGCTGCGTGAACCTGGTAATAAAATT	62640
QY	8544	cgaccctcgacctaaacactggtgtatctatagattcacacacattgtatgaaagacat	8603
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QY	8604	tgtgaatctctcgltctgttctgttlltaacatggtgacacacagtgctcacagccctgtca	8663
Db	62701	TGTGAACCTCCCGCTTCTATTCTGTTTCACTCTGTCCATCGGCTGCTCAAGCGCC-GTCA	62759
QY	8664	cgtaacccctcgcttaccatccgatccgaacccctctatgaaagccccccttagagttgt	8723
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QY	8724	gagcccttaaaaggcagaagttgagcacacttgacagagctcggattttgaaagcgtacgc	8783
Db	62820	TAGTCTTAAAAAGGACAGAAAGTTGAGACACGTAGAGAGAGCTCGAATTTTAAAGCGTAAAGC	62879
QY	8784	tgcgcattctccacagctaataaagccacactcccttcacatctcgtgtctgaagggctt	8843
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QY	8844	tgtctcagctgtcctcgtctacacgtctcagcta	8876
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RESULT 7			
HSJDJ636H5			
LOCUS	HSJDJ636H5	116679 bp	DNA
DEFINITION	Homo sapiens chromosome 1 clone RP4-636H5, *** SEQUENCING IN		
ACCESSION	AL21602		
VERSION	AL21602.1	GI:6002330	
KEYWORDS	HTG; HTGS_PHASE1.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
AUTHORS	Eutheria; Primates; Carnivora; Homiidae; Homo.		
TITLE	1 (bases 1 to 116679)		
JOURNAL	Direct Submission		
COMMENT	Submitted (29-SEP-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humbrey@anger.ac.uk Clone requests: clonerequest@anger.ac.uk IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished: dj636H5 Contig_ID: 00009 acc- length: 10033 bp Unfinished: dj636H5 Contig_ID: 00013 acc- length: 3796 bp Unfinished: dj636H5 Contig_ID: 00014 acc- length: 1463 bp Unfinished: dj636H5 Contig_ID: 00015 acc- length: 3590 bp Unfinished: dj636H5 Contig_ID: 00016 acc- length: 3490 bp Unfinished: dj636H5 Contig_ID: 00017 acc- length: 5077 bp Unfinished: dj636H5 Contig_ID: 00018 acc- length: 5077 bp Unfinished: dj636H5 Contig_ID: 00019 acc- length: 1090 bp Unfinished: dj636H5 Contig_ID: 00020 acc- length: 5538 bp Unfinished: dj636H5 Contig_ID: 00021 acc- length: 1293 bp Unfinished: dj636H5 Contig_ID: 00022 acc- length: 3366 bp Unfinished: dj636H5 Contig_ID: 00023 acc- length: 2086 bp Unfinished: dj636H5 Contig_ID: 00024 acc- length: 4631 bp Unfinished: dj636H5 Contig_ID: 00025 acc- length: 1546 bp Unfinished: dj636H5 Contig_ID: 00026 acc- length: 3784 bp		

QY	2626	gcctggagatcccaaccagccagagtgacgcgagctctcgagagctctccctgggtgagccat	2685
QY	2566	gattacagagatgctcgaggcagcctccttgagcggttttaagcctgcgccttggaaacatccc	2625
QY	54111	GACTGAC-----GCGCGGCTTAACTGGCCCTGTGAGAGGTGCC	54149
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QY	53931	GAGTTGTGAGCCCTTAAAGGACAGGAATTCCTCACTCGGGGAGTTCGAAATTTAAGGC	53990
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QY	2386	gggttggtgagcccttaaaagggaacgaagttagatcagacgaagctcgtgatttgaagc	2445
QY	53931	GAGTTGTGAGCCCTTAAAGGACAGGAATTCCTCACTCGGGGAGTTCGAAATTTAAGGC	53990
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QY	53991	ACTAGCTTCGCGATGCTCCACAGATGAAATTAAGCCCTTCCTCTTACAACTCGGTGCTGAG	54050
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QY	53872	CCTGTACGTAACCTCTGCTGTCTGCTCAAAATCAATCAACGACCTTTCAATG-TGAATTCCTTA	53930
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QY	53931	GAGTTGTGAGCCCTTAAAGGACAGGAATTCCTCACTCGGGGAGTTCGAAATTTAAGGC	53990
QY	2446	gatacgccttcagatctcctcagactatlaaagcaactccctcactatctcgtgtclta	2505
QY	53991	ACTAGCTTCGCGATGCTCCACAGATGAAATTAAGCCCTTCCTCTTACAACTCGGTGCTGAG	54050
QY	2326	ccgttcacgttaccctccttggtcttactcaatcgcatacgaaccctctcatgcggaacccctta	2385
QY	53872	CCTGTACGTAACCTCTGCTGTCTGCTCAAAATCAATCAACGACCTTTCAATG-TGAATTCCTTA	53930
QY	2386	gggttggtgagcccttaaaagggaacgaagttagatcagacgaagctcgtgatttgaagc	2445
QY	53931	GAGTTGTGAGCCCTTAAAGGACAGGAATTCCTCACTCGGGGAGTTCGAAATTTAAGGC	53990
QY	2446	gatacgccttcagatctcctcagactatlaaagcaactccctcactatctcgtgtclta	2505
QY	53991	ACTAGCTTCGCGATGCTCCACAGATGAAATTAAGCCCTTCCTCTTACAACTCGGTGCTGAG	54050
QY	2326	ccgttcacgttaccctccttggtcttactcaatcgcatacgaaccctctcatgcggaacccctta	2385
QY	53872	CCTGTACGTAACCTCTGCTGTCTGCTCAAAATCAATCAACGACCTTTCAATG-TGAATTCCTTA	53930
QY	2386	gggttggtgagcccttaaaagggaacgaagttagatcagacgaagctcgtgatttgaagc	2445
QY	53931	GAGTTGTGAGCCCTTAAAGGACAGGAATTCCTCACTCGGGGAGTTCGAAATTTAAGGC	53990
QY	2446	gatacgccttcagatctcctcagactatlaaagcaactccctcactatctcgtgtclta	2505
QY	53991	ACTAGCTTCGCGATGCTCCACAGATGAAATTAAGCCCTTCCTCTTACAACTCGGTGCTGAG	54050
QY	2326	ccgttcacgttaccctccttggtcttactcaatcgcatacgaaccctctcatgcggaacccctta	2385
QY	53872	CCTGTACGTAACCTCTGCTGTCTGCTCAAAATCAATCAACGACCTTTCAATG-TGAATTCCTTA	53930
QY	2386	gggttggtgagcccttaaaagggaacgaagttagatcagacgaagctcgtgatttgaagc	2445
QY	53931	GAGTTGTGAGCCCTTAAAGGACAGGAATTCCTCACTCGGGGAGTTCGAAATTTAAGGC	53990
QY	2		

Db	54150	TCGGGGGCACTCCAGACAGCTTGAGTGAAGCC-GATCCAAAGAGTGTCTCCGGGTAGGCA	542083
QY	2686	ttgcccggttggagacactcgcgcagaagcagtgltgtgcaggcccccgttggagatcaaca	2745
Db	54209	TTGCCCCAGTGGAAAGCGCGTCGCAGAGCGACATGTAGCGAGGCCCCACAGAGATTAA	542683
QY	2746	gaatgtctgaacacccgggaggaatttggacttgaagtcgcgcggaacataaacttggtaa	2805
Db	54269	CAGTGGCTGAAACACAGAGAGAACTGGGCACCTTGGAGTCCGGACATCTTAAACTTGGTAA	543283
QY	2806	gactagctcttggaaacttgcacactccatccacactccatttgaatgaaagatgctgtatccacag	2864
Db	54329	GACTAGTCTTTTGGAACTTCCCCACATCCATCTGAGGGAAGACATGGCCGTGATCACCATG	543883
QY	2865	gggtgcctttatcaacgacttggtttggtttgaacttggtttgaattacttgaacggact	2924
Db	54389	GGGGGTCTGCATATGGCACTTTTG-----	544123
QY	2925	ggtcttggaaacttggccactccatccactccactccatttgaatgaaagacatgctgactc	2984
Db	54412	-----	544123
QY	2985	gatacccaacgagtgctgctgtccggcacttggtttlttgttttgaacttgaactatc	3044
Db	54412	-----TTCTGGTTTAACTGTGACTTGAAT	544383
QY	3045	gcttgaacttgggttggtttgaacttgcctgctgcttgaattccgaataactcgaatttgt	3104
Db	54437	GCTGGATACCTTTGGTTTGGTTTGTACTGTCTTGATTTTGGTACTCGGAATTTTGA	544563
QY	3105	tt---tgatttggtttaagtgaacatgcgaagaatgtgtgcgtccctttaccgcttc	3161
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QY	3162	tttgttttgggt---gtgcattgtgtgtagaagtgtgtgtgtcctcgaagaacatgt-	3219
Db	54557	TTTGTCTTGTTGTTGATGTGTGTGATGTGAATGGTATTTTGTATCAAAAAAATAAAC	546163
QY	3219	-----gtcagcgacaataaagccacccacactacagaaactatgttga---aatcca	3269
Db	54617	AGCATGGGTGACAGCAAAATAGCCCAACCCACATAGAAACATGTATAAAGAAATTTCA	546763
QY	3270	gaagagatttgaaggagattacggtgttactatgacataagaataaactagaacttgt	3329
Db	54677	GAGAAATTTTAAGGGAGATTAGCGGTACTGTGCACCGAGAAAACTTTAAACTTTTGTG	547363
QY	3330	taaatatagactgccaacacttgaaggtgtgttgcacatcagaagaagactgaacaggtc	3389
Db	54737	TGAATTAGCTGACAGCATTTAGAGTGGTTG-----GCCTGGACAGTTC	547823
QY	3390	ccttgtttcaaatgtatgycacaaggttaactgttaagccaagycacacagacagttct	3449
Db	54783	CGTTGTTTCAAAAGTATGACAAAGGCCACCTGTAAAGCAAGCAACCCAGACACAGTTCT	548423
QY	3450	gtacgtataacaattcacgctgtgttttagaccccttgcgcccccaagtatgtaaaga--	3508
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QY	3508	-----	3511
Db	54903	AGCAGCATTAATGGCCGGGACGCTGGCTCAAACTGTATCCAGACATTTGGAGGGCG	549523
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Db	54963	AGGCGGGCGGATCAAAAGTCAAGGATTCGAACCATCTCTGCTTAACACGGTGAACCC	550323
QY	3572	gaacagaagctcaaaagagagaaagaaatagaga-----	3606
Db	55023	GTCTCTACTTAAATAATCAAAAAAATAATTAGCTGGCGCTGTGTGGCAGGCACTGTACT	550823
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QY	3712	gtaacacttaatacact---ttgtgttagtvttaacaaagggcgfat-----	3758
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QY	4078	ggcctcctgaatctatttgaagaaacagtttatgtgcaggtgcaaaagtaaaat	4137
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QY	4138	atactttgtgcaaaaagtttgaaggaagcataagaatgtgatttttaaccttaataa	4197
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QY	4198	aggttaaaaaaatattgttt-----	4219
Db	55803	ATTATATTATCATTAATTTGGGTGTTCTCTCTCAGAGAGGGGATTTGGCAGGGTCATAGG	55862
QY	4219	tgaagtttaagcaagttttaaatgttaattgttaaaaaaaatctgttgttaactaa	4278
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QY	4279	ttagttaaagtaaaagtgtaacacaggttttcttgyaactgagct-----	4328
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	Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 162921)			

TITLE	Direct Submission
JOURNAL	Submitted (03-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire CE10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
COMMENT	Reqs 3, 1999 first sequence version replaced g1:6165528.

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Contig_ID: 00021 Length: 16812bp

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Contig_ID: 02646	Length: 1999bp
Contig_ID: 02654	Length: 1435bp
Contig_ID: 02690	Length: 6013bp.

* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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DEFINITION Homo sapiens clone NH0085M14, *** SEQUENCING IN PROGRESS ***, 30
unordered pieces.
ACCESSION AC012487
VERSION AC012487.1 GI:6137956
KEYWORDS HTG: HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 191235)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 191235)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT
* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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FEATURES
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Best Local Similarity 68.1%; Pred. No. 0;
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QY	6362	accctccacagacgcgagaaactggtcccaagatatacatcaagtaactgaagtgagcaaa	6421
Db	106350	ACCTTCCTCAAGACCGAGGACTATTCACAGGGTATACAAACAAGTCACTGAGGTAGGACAA	106409
QY	6422	agattgtctacagttccattatttcaatggtataataagtgtagcagaagctctaaagaa	6481
Db	106410	AAGTGTGCTGCGCTCTATTATTTTGTGGTATTTAAGTGTACTGCAACTCTAAAGAAGAA	106469
QY	6482	ctttgtgtataatagcattctctacaaaggtatgtacccgaagaaataaaccaacctgagt	6541
Db	106470	CTTGTGTATTAAGTATTCTTATACAGGATGTATACCCAGGAAGAAAGACCAACCTGTAGT	106529
QY	6542	tgttataagccattttaagccctcccaatgatcacagttctttaaaataaatgaagact	6601
Db	106530	TGTGTATGAGCCACTTC-C-ACCCTCCATGACCCACATTTTAAATTAATTAAGACCT	106588
QY	6602	ggtccct-----ttctagtgtagcacagaatgaagtaatagctaaagacagaagaaga	6652
Db	106589	GAGGACTGTGTGGGGCTCATTAAGATACGAGTAGTAAGTGTACTTAACAGAGAAGAAAA	106648
QY	6653	gggtgccccaagcgtgtacaactaaatttaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	6712
Db	106649	GGGGTGGCCAAACAAGTACCTTAAAGTTAATGTCTGCCCTGTCTATTATAGTAAATAG	106708
QY	6713	catagaataagatgcgttctcttaactgtgaaaaaaaagaagtacacagcagaagataa	6772
Db	106709	TTAGAATTAAGCTGTGTGTCTTAATT---AGAAAAGAGGGCTATTTGGCAGAAAAATA	106764
QY	6773	gtatactgtccacgaattaaagctcagtgccaaatggtgttaattactcgtgtgtgtcat	6832
Db	106765	GTACATCTGTCAATAATTAGACTGTGTGAAATAATAATAATACGTGCTGTGTCTCA	106824
QY	6833	cttaggcctacttag-aaaaagagtagaaagaaccgtgtgtgtgtgtgtgtgtgtgtgtgtgt	6891
Db	106825	TTAAGCCACTTAGAAAAAAAATGTAATAAAGTCCAGTCCACTTTCATAAAGGAAAAAATG	106884
QY	6892	ggccctcctgtacagtagagaaagctgcacaaccctctgaattagtaattatcacatcccttaa	6951
Db	106885	GGCCTTCTCTGTACTTAAGGGAACAATGTAAACCCCTTAGAGCTAGTAATAATACCAATCCCTTG	106944
QY	6952	acccaaggtagaaaaaaagaagtcacagttatctctgtggcgtcgataaaaaagactagat	7011
Db	106945	ATCC-TCGCAGAGAAAAAGAGGACAGTGTGCCTTAAGAAATCGACGGGCGGCACTGGAT	107003
QY	7012	cgtagagtaaatctactgaataaagaggaggtgtgtgaactctctccggacagactttt	7071
Db	107004	CCTCAAGTAACAATCTTAGTTTCGAGGGAAGATTATTAATGCTCTCTTAAGCCAGTGT	107053
QY	7072	cagaacttctatgataactaaatggtgcagttacagagaactccaggaagaaacacagaat	7131
Db	107064	TAACTTCTATGATGAACATAATGTGCCAGTACCAGAATAATTCAGSAAAAACAAGAAAT	107123
QY	7132	ttgtttttgcaattagccgagcatgttagcccaagtctctaaatgtagcttaactgttcaact	7191
Db	107124	TTGTGTTTGGCAATTAAGCCGACAGCATGTAAACCAAGTCTCTCATATGTCACTTACAGCTATGTA	107183
QY	7192	tgtggagaaactgtatgaataagatcaaatgg-cataaagaagccgagaagtaagtgctctac	7250
Db	107184	CGTGAGAAACTGTAAATGAGATCAATGGCCACAGAGAGCCCAAGATTAATGTAAGTCTACA	107243

QY	7251	gaaccagttccctgatagtatcccgccccaagaataccctgtacatcttcttgatgtctca	7310
Db	107244	GACCCAAAGTTCCTGATGGAATTCGCCAGCTCAAAAGAAATACCCCTATATATTTCTTGAGCTTA	107303
QY	7311	aaagctcaatattatagaacaatttgtatagctgtgaaaaaggaagaattcactcaacct	7370
Db	107304	AAAGGCTCAATATATTTGGCAATATTTGATGATAGCTTAGAAGAGAAAGAAATTCACCTCACACC	107363
QY	7371	gtagaataccttagttgcctctagagcaaaaactgtataatgttaccacaaaaacagttaca	7430
Db	107364	GTAGAGTATACCTTAGTGTGCTTAGACAGAAAGTGATATATATGAGCAACCAAAAACAGTCACT	107423
QY	7431	tggtgagttccaacaccacacagataaaatccatctcagtaatttccaaagttgcagacc	7490
Db	107424	TGTGTGAGTTCTCAAGTCACACAGAGAGAAATTCATTGTAGTAATTTCCCAAGTTGCAAACT	107483
QY	7491	gtttaagcccaacccegaattccaccgggacttagacagccccccactagctatacctgagt	7550
Db	107484	GTGTGGACCCACCCGGAGTCCACCGGAGCTGGACAC-CCCCACATAGATGTATCTGGAGT	107542
QY	7551	acgtgagacatagaacactcagctaaagccgcctgaccagtgagcaagtgatgtgttctatg	7610
Db	107543	ATGTAGGATATGAGCTTATGCCAAATTACCGAGCACAGCAGAGAGTGTGTACTGG	107602
QY	7611	cactatlaaacacatcttctctcctactgcgcacatacaatagcgaactccctggctccc	7670
Db	107603	CACATTTAAACCACTTTCTTCTTACGTGCCATTAATAACAGGGGAAATCTTAGGCTTCCC	107662
QY	7671	tgctatgcttccgcgcgaaaaagcgaacatagcccatgataatataaagaatgataatg	7730
Db	107663	TGTCTATCTCTTCCACGAAAAGAAACACATAGCTATAGAAATGTGAAMCATATTAATG	107722
QY	7731	accaccctaa-aaaattatacaatctctagagccgcgcacacttagacaaagaatggctcatg	7789
Db	107723	GCCTCTTAAGAGAAATCATGCATATTTTATAGCCGTGCTACTTAGGCACAAACGGCTGCTG	107782
QY	7790	ggtataccagaccccccattcatagctcacaactgatatatacgggttgcaagctgtttaga	7849
Db	107783	AGGATACCAAGACCCCATTTGCATGATCACTGAATCATAGCGGTATCAACCTGCTTAAA	107842
QY	7850	aatcataactataaacaacagttcaagccttgacatctctggcccggaagaacctaagat	7909
Db	107843	AATAACCACTATAAAATGGCAGAGCTTGACTCTTGCGCCGGAAATAAATCTAGAT	107902
QY	7910	aagaatgctatctcatcaaaatagattggctctgcgactact-ctagcagctgaagaag	7968
Db	107903	GAGAAATCTTATCTATGCAATTAATTAATTAAGCTCTGACTACTTGTGCAGACACTGAAGTGA	107962
QY	7969	ggtctata-aaaatttaaccttactaatctctgtctacacatagataatcaaaagcaagt	8027
Db	107963	GGCTGTGTGGAAATTTTACCTACTAATTTACTGCCCTATACATAGATATCAAGGCAAGT	108022
QY	8028	agttaaagacgttagtttaaagcacatagttaaaaacaatgacaaaactggcaatgtgcggt	8087
Db	108023	AGTTAAACACATAGTTTACAGATATA-----ACAAATATGACACATGTGCCGT	108070
QY	8088	acgagttgtagacaggtatcgacccctgagacgattttaagaagtggtgtcccaagcttagg	8147
Db	108071	ACAAATGTGGCATGATGATTGATCTGTAGGCGCATTTTAAAGAAATGTTGCCACACTACG	108130
QY	8148	aggaattaaacctttat-ataggagtataatagtaataagaacctgtctactgtctccc	8206
Db	108131	AAGATTTTAAACTCTTATATAAATAAGTTATATGTATAGTAAGGAACCGCTTACTGCTCCC	108190
QY	8207	ttgctctgtgcctgtactcttctcaaaatgataaaagttcatctgtctactcttagttacca	8266
Db	108191	TTGTTTGTCTACTGTACTTCTTCAAAATGATATAAAAGTTTATGTGCTTACCTTAATTACCA	108250
QY	8267	aaatgccccaacaacagtgatctatatgtaatcaacttcaactatctatgcaaaagaagcat	8326
Db	108251	AAATCTCTTACACAGAAAGTGTAATGATGATGAAATCACTTCGATCTGTCTTCGAGGAAG	108310
QY	8327	aagtgtgcaaaaataagatgtgaagatcccccactaaataaagvtgagagttcacaagcgggg	8386

Oy	2900	ttgttgtaatactatgcagagaccggtccttggagaaacttgcacactccatccactccaa	2955
Db	54952	-----	54952
Oy	2960	tttgatgtaagacatgctcgtatcatcaccacagctgtgcctgttccgycactttgt	3019
Db	54952	-----TTTGGT	54947
Oy	3020	tttgttttttgacttgtaacttagatctgtatgaactttgttttggatttgaccctgtctg	3079
Db	54946	TTTTGTTTTTGACTGTGACTGTGATGCTTGATACCTTGGTTGGTTTGGTTTGACTGGCTAG	54887
Oy	3080	gatttcgaatcactcttgattttgtgttttgattttgttttagatgtaaacctgcagaaagtctg	3139
Db	54886	GATTTCTTGATATTTGTGACTTTGGTTTGATTCTGTGGTTGATTAACGTGAAGAGTGIG	54827
Oy	3140	tgcgtgcctcttttaaccctcttccttctgttttctgtgtgtgtgcattgtgtgtagaagtgtct	3199
Db	54826	TGTGTGCCCTTTTACGTGTTCTTTGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	54767
Oy	3200	ttgtctcgaaagaacatggtgtcagcacaacaa-taaagccaccctcctagaacctgtgtg	3258
Db	54766	TTGTCTTGAGGAGACATGGGTGTCAGGCACAAATAAGCCCAACCCACAGAGAACTATGTGG	54707
Oy	3259	aaaaattcacaagaaggttttaaggagatgcaggtgttaccatatacctagaaaaaact	3318
Db	54706	AAAAATTTCAAAAAAGATTTAAGGAGATTNAGGTTNAGGTTACTATGACACACAGAAAACCT	54647
Oy	3319	agaactctgtgtaaatatagactctgcacaacattagagttgtgtgttgcacatcagaagaagc	3378
Db	54646	AGAGCTTTGTGTGAATATGACTGGCCAGCATATAGAGTATGTTGGCCATCACAAGGAAGC	54587
Oy	3379	ctagaacaggtcccttgtttcaaatgtatgtgcacaagtaacctgtaaagcagaagcacaa	3438
Db	54586	CTGCACAGTCCCTGTTTCAAAAGTATGCGACAAATGTAACCTGTAAAGCCAGCACCA	54527
Oy	3439	gaccagcttctgttaagtatgaca-----attacagctgtgttttagaccctc---ttgcctc	3491
Db	54536	GACCGATTCCTGTATATGACACTTGGTTACAGCTGTGGTTTGAACACCCATCCCGGCC	54467
Oy	3492	cacagtagttaagagaggcacagaagaagagaagaacagagacaa-----	3537
Db	54466	CACAGTGGTTGAGAAACACAGCAGCCTTAAGTGGCTGGCAGAGCCAAAGAAACAGCAGG	54407
Oy	3537	-----aaggaagctcaaaagagagagagagagagagagagacagaa	3578
Db	54406	GAGAGAGAGAAAAAGACAGACAGAGGAAAAAGACAAAGAGAGAGAGAGAGACAGAG	54347
Oy	3579	agtcacaagagaaaaaatalagagagaatalatccaagtatgta-----agaa	3627
Db	54346	AGACAAAGAGGAGACTCAAGAGAAAGAGAAAGAGAAAGAGAAAGATATACAACTAGTT	54287
Oy	3628	aaaaatagtatgacctatctccctttaaagaagccaagttaaatattaacctaataatgtata	3687
Db	54286	AAAAAAAGTGAACCTTATT-CATTTAAAAAGCTAGGGTAAATTTAAAAAAGCTATAATTTGATA	54228
Oy	3688	attaaagtatctccgttaaccctgttaaaccttaacctaatacacttgtgttttagtttaaac	3747
Db	54227	ATTGAAGGCTTCTCTGTGTGACCCCTTAAACACTTCACATACCACTTGTTGTAAGTGAAC	54168
Oy	3748	aagggcgtatcccgaaagcactgag-----gacctccatcaaaaaaalc	3790
Db	54167	AATGACATATAGCCCGAAAGACATGAGGCCACACTCAAAACCTGCAGCCTTCTCATCAAAAATC	54108
Oy	3791	cttaaccagtaecccaegatgtgccagatgtcatcattcaactctgttagcagcagctgtcttg	3850
Db	54107	CTTAACCCAGTATACAGCGGATGGCCCAATCATCTCATCTGTAGAGCAACTCCTTTG	54048
Oy	3851	ctaaacagaaaaaagaaagagagcgtgtgtaagagcacaatattatgttaaaagaagtg	3910
Db	54047	CTTACAGAAAGATGAGAAAATAACTTTTAAGCAAACTCATGTGTGTGATGCACCTCAC	53988

QY	3911	tatagtgtaaatctctgctctgtaaatattaaccgctgttttaagaagaagaatacttctg	3970
Db	53987	CAGTTCAGAGTATTTCTTAAGTAAAAA-----AAAAAAGAGATTTTGC	53934
QY	3971	aataagtcagaagctgtagacatgctcaagaatctacctcgaaagtcatag---aaacg	4027
Db	53933	AACAGTCAGAAAGTTGAGGCATGTGCAAAATATTCGTGTAAATTTGTGGAAAAAAG	53874
QY	4028	atgctataaaaaattatgcaaaaaatctgataaattgaaagtaaaagccctcga	4087
Db	53873	GTTATAAAAAGATTTATGCAGAAATCTGTATATTTAAAGCAGACAGCCCTCGA	53814
QY	4088	gt-----actatggaagaacgctttatgctgaagctgcatagaagaagtataatact	4142
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QY	4203	aaaaaaatatctgtttgaaagtttaagccaagttttaaaagtttaattgtaaaaaaat	4262
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QY	4263	tctgtgtttaaactaatagcctaaagaataaaaggatcatccagttttctgtgaactg	4322
Db	53636	TCTGTGTAAACATATTAGCTTAAAGGTTAAAGGGTGTCATCTAGTTTTCGTGCACTG	53577
QY	4323	gacattaaagtaaaaatgcaacaggttttctctggaagcacaacctgctcttaaaaaa	4382
Db	53576	GACATTTAAAGTAAACACAACTAGGGTTTGTGTAAAGCATTAACCTGCTTTAACAAAG	53517
QY	4383	attataaaaggtttaaagaagctgttaaaaaactaactatgcttaagtaacatgaaaaattg	4442
Db	53516	ATTATAAAAAGGTTAAAGAGTTATATAAAAACTTATCCTTATAGTGCCACATTAAAAATGG	53457
QY	4443	gttaaatgtctagagaggttttatataaatgaatttaacattaaataacacataaat	4502
Db	53456	AATTAATATGTGTACAAGGTTTATTTAAACTAAGTTTAACTTATATACACACTAATAT	53397
QY	4503	aaaagtaaaatttagcttatactctgctgataaaaaatcaacaagaagatattataatataa	4562
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QY	4563	atggtgttagcttctcttctgtctaaaaactaataaaataggtctcaaggaa-----	4617
Db	53336	ATGGGTGTTT-GTCTTCTTGTGCACAAAAACTAATTAAGATGATGCTTAAGAAATTTCT	53278
QY	4617	-----	4617
Db	53277	CAGTAGAAAGGACCCAGAGACTATTAAGTCCACTTCTGATGCCACATTTAAAAACAA	53218
QY	4617	-----	4617
Db	53217	AGGTAAAAATATATTACTTATTTATCTTCACCTTCTCTTCCCTCAAACTAAAGTC	53158
QY	4617	-----	4617
Db	53157	TTTATGACATGTACCACCCCTAGAAATTTCTGTAAACAGACAGACAGCTGAAGATCACAT	53098
QY	4617	-----	4617
Db	53097	TCTCATCAAGGGTAAAGAAAGAAAGAACTGAGCCAGCCTAGNAGACACTACTTGT	53038
QY	4617	-----	4617
Db	53037	GCTGCTAACCAACGAGACTGCTATTCTATACAGCAAAAAAAGATGACTCATCACACCG	52978
QY	4617	-----	4617
Db	52977	AGTCAAGAAAGGCCACCCCTCCAGATTCGTGGGCCATTAGTCCAGGAGAAACTATAC	52918
QY	4617	-----	4617

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QY 4617 ----- 4617
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Oy	6334	atacataagtcactcgaggttaggacaaaaagatgctacagtcctattatcttaatggttat	6453
Db	50945	ATACATCAAGTCACAGAGGTAGGACAAAAAGTGGTACAGTCCATTAATTTATGGTAT	50886
Oy	6454	tataagctgacgagaccctaaagaacctgtttgttataagctatccataccaagta	6513
Db	50885	TATAGGTACTGGGACTCTAAAAAGAACTTTGTGTATAAGCTAATCTATACAGATA	50826
Oy	6514	tgtaagcctaggaaataaaccaacctgatactgtttatgaagcccaattaaagcctcaatgat	6573
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Oy	6574	caacgcttttctaaataaantaagacgc-----gtcctttctagtgagacacaag	6624
Db	50766	CACACTTTTTTGAAAAATTAATAAGGCTGAGAGCTGTGGGGGCTATTAATGGTATGAG	50707
Oy	6625	taaagttaagctaaagacagaagaagaggaatccccaagcattgaacataaattaa	6684
Db	50706	TAAACTGTATGCACAACAGAAAGGAGGGGTGGCCAAACAGACCTGTAATTTGA	50647
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QY	7524	acagcccccaactagagctatctcgtgtacgttgacatagaactacgcctaacgcgtcga	7583
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QY	8061	catcacaaaactgcacatatcgtccgttagagtgtagacagatcgcgccttgagacat	8120
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QY	8121	gtttagaaggttgytccccaagcaccttagaggaattiaaaactctat-ataggagtataat	8179
Db	49244	GTTTGGAAATAGTGTCCACAGGCTAGAAAGATTTAAACCTTATATAAAGATTATAT	4918
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QY	8420	tttatattgttttatactc--agaaaagtagagagaagcgaactaaagggaggtagccc	8477
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QY	8658	cgtaacgacaccccccgggttactcaatatgatacagacccttcacagagaccoccting	8717
Db	48725	CCAGTCATGTACCCCTGCTGCTGCTCATGTGATCAACACCTCTCAATGTGACTCCCTTAG	48666
QY	8718	agttgtgagcccttaaaagggcagaagttgagacaccttcagacgtcggatttggagc	8777
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QY	8778	ctagctgcgcgattctccagctgtatataagccaatcccttaactatctcgtgtgttg	8837
Db	48605	TGAGCTCTCCCATGCTCTCTGCGCAGATTAACCCCTTCCTTTTAACGCGTCTGAG	48546
QY	8838	gggtttgtctgagctgtgctcgtcaactctgag	8873
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DEFINITION	Homo sapiens clone NH0218F06, *** SEQUENCING IN PROGRESS ***	2	
ACCESSION	AC010877		
VERSION	AC010877.2		
KEYWORDS	HTG; HTGS_PHASE1.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 138088)		
TITLE	Waterston, R.H.		
JOURNAL	The sequence of Homo sapiens clone		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 138088)		
TITLE	Waterston, R.H.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (25-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA		
COMMENT	On Nov 2, 1999 this sequence version replaced g1:5923733.		
	* NOTE: This is a 'working draft' sequence. It currently		
	* consists of 2 contigs. The true order of the pieces		
	* is not known and their order in this sequence record is		
	* arbitrary. Gaps between the contigs are represented as		
	* runs of N, but the exact sizes of the gaps are unknown.		
	* This record will be updated with the finished sequence		
	* as soon as it is available and the accession number will		
	* be preserved.		
	* 1 66357: contig of 66357 bp in length		
	* 66358 66375: gap of unknown length		
	* 66376 138088: contig of 71713 bp in length.		
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	/db_xref="taxon:9606"		
	/clone="NH0218F06"		
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Query Match	10.6%: Score 2644.2; DB 43; Length 138088;		
Best Local Similarity	67.8%: Pred. No. 0;		
Matches 5345; Conservative	0; Mismatches 998; Indels 1542; Gaps 56;		
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QY	2111	gaatataagcagatagccgcgcgccttagaacaacagaccgaagcctgycctg	2170
Db	16667	AAGGAAGTAAATTCAAAGACAGGAGCCCTGGACACAGGCTCTAAACACAGGCTGGGGCTG	16726
QY	2171	cctgaccctaagctcgtaattaaatctgaccctccgacctagcaactgtgttactata	2230
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QY	2231	gattccagaacattgtaatggaagggatgtatgaaaggaacatgtgaaatctcgtttc	2290
Db	16787	GATTCACAGA-----CATGTATAGAAAGAACACTGTGAAACTCCCTGACCTT	16831
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RESULT	LOCUS	DEFINITION	LOCUS	DEFINITION
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		Homo sapiens chromosome 6 clone RP3-383p5, *** SEQUENCING IN		
		PROGRESS ***, in unordered pieces.		

ACCESSION	AL121947
VERSION	AL121947.2
KEYWORDS	GI:6249384
	HTG; HTGS_PHASE1.

ORGANISM	Homo sapiens
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 144304)

AUTHORS	Slms, S.
MITT D	Direct Cubic

TITLE	Direct submission
JOURNAL	Submitted (03-NOV

Cambridgeshire, C

COMMENT

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on Nov 4 1999 this sequence version replaced gi:5065993.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E. coli, yeast, vector,
phage etc. Order of segments is not known. 800 n's separate
segments. Unfinished: dj383p5 Contig_ID: 00075 acc-AL121947
Length: 5485 bp Unfinished: dj383p5 Contig_ID: 00226 acc-AL121947
Length: 22864 bp Unfinished: dj383p5 Contig_ID: 00295
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00641 acc-AL121947 Length: 7093 bp Unfinished: dj383p5
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01522 acc-AL121947 Length: 5549 bp Unfinished: dj383p5
Contig_ID: 01640 acc-AL121947 Length: 6069 bp Unfinished:
dj383p5 Contig_ID: 01720 acc-AL121947 Length: 5056 bp.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

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FEATURES

Location/Qualifiers

Source

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/chromosome="6"
/clone="RP3-383p5"
/clone_1bp="RBC1-3"
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ORIGIN

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Best Local Similarity	69.3%;	Pred. No. 0;		
Matches 4901;	Conservative	0;	Mismatches 824;	Indels 1347;
				Gaps 50;

[illegible]

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OY 4367 ctgctcttaacaaaattataaagaaggttaaaagaagctgtaaaaacttactatggt 4426
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QY 6983 cctcgggcgtcgaataaaaaagagactagatcctagagtaaatactagtaaaaaagagag 7042
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QY 7163 agctctaaatgacactaatgtttagcttgttgagaagaactgtaagaatgaatgaatg- 7222
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OY	7281	aagaatccaccctgcatcattcctcaggtctcctcaaaagtcctcaattattagacaattgcata	7340
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Db	23354	GCAAGAGTAGAGGAAGACTTCAACCCCTCTGTATAGAAAGACTACAGCTGCTTAGGCAAAAAA	23295
OY	7401	ctgtataatggtaccacaacaaacagtttaaatggtgaggtctcaaacacacagataaat	7460
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OY	7461	ccattccagtaaatcttcocaaagctgcagacccgtttaagccacccagaattccaccggagac	7520
Db	23234	CCATTTAGTAATTCOCCAAAGTTGGCAACCATGTATGATCTCTCCAGAGTCCACCGGAGAC	23175
OY	7521	tagacagcccccactaaggctactgtaacgltgagacatagaaacctacgctaagctcc	7580
Db	23174	TGGACAG-CCCCCAGCTGTATTATACGGGATATGTAGGCGATATACCTTATGCCAAATATACC	23118
OY	7581	tgaccaagtgagaaagtaagtgtgtatgtgacatttaaacatctcttcctctactgac	7640
Db	23115	TGACCAGTAGAGCAGGATAGTTGTATTGGAATTATTAACCATCTTCTTCCATCTGGC	23055
OY	7641	catacaatatagagcgaactcctctggtctccctgctctatgctcttcgcggaagaacgaaacat	7700
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OY	7701	agccataataattaaaaatgataatgataatgacacct-aaaaatatatacactatag	7759
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OY	7940	tctgcagcactt-ctagcagctgcgaagaaggtctat-aaaaattaaaccttaccatata	7997
Db	22755	TCTGCACACTTGTGCTACTGCGCTGAAGGAGGGGTTGTGGAATAATTTAACCTTACTATATG	22696
OY	7998	ctgtctacacatagataaatacaaggcaagtagttaaagacgtagttaaagacatagttaa	8057
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OY	8058	aaacatgcacaaactgcgcacataatcccgctacgagltgacaggaattcgaccctgaagc	8117
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OY	8118	catgtttgaaggtggtgtcccgacacatagagatttaaaactctat-atagsgattat	8176
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OY	8177	aatagtaataagaacctgcttaactgctccctgctgctgcagcctgtactcttcaaatgat	8236
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Db	22408	TCATATCATCATATTATTGCGACAGAGAGCTAGTAGTGTGAATAATAGAGTGAACACTGCCA	22349
Qy	8357	ctaataaaagttagagagctcacaacggyggaatgaagga--agagagagcccttcac	8414
Db	22348	CTAATAAAAAGTAGAGAGTCTCAAAAGTGGCGGAATAGAGAACAGAGACAGACCCCTCAT	22288
Qy	8415	atgttttatatatgttttatacttcgaaagaacagagagagagaaactaaagccggttg	8474
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Qy	8475	ccgcgcgcctaagaaccagaccg-----aaaccagccttgagcc	8514
Db	22228	CCCCGCACTTAGAACAACCAACCCAAACCAAGAAACCAAGACTTAAACAGGCGCTGGGCG	22165
Qy	8515	tgccctgaacctaaagcctgtagttaaataatcgaccctcgaccctagaacatggtgttatcta	8574
Db	22166	TCCCGTACCTTAAGCCCTGGTAGTTAAATTGACCCCTGCACCTAGGAAAGAGATGTTATCTA	22109
Qy	8575	tagattccacacattgtagagaaggaacattggaatcctcgtctcgtctgttttcaact	8634
Db	22108	CAGATTCCAGACATTTGTATAGAAAGACATTTGGAAACTTCCTGGTCTGTCTCTTTCACT	22049
Qy	8635	gtgacacaacagtgtctcaacagccctctgtaacgtacccctcgtactcaatcgatcaaga	8694
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Qy	8695	ccctctcaatgaagacccctttagtcttgtagcccttaaaagsgaagaattgagcaact	8754
Db	21989	CCCTCTCACATGAGGCCCATAGAGTTGTGA-----	21958
Qy	8755	tgaagagctcggattttagaagcgtacagcctcggaattctccagctgattaagccaatc	8814
Db	21958	--ACGAGCTCGGCTCTTGAGAACAGAGCTTCTGATGCTCCCGGCCAAATTAACCCCTT	21901
Qy	8815	ccctacacatcccggtctgctgaggggttttgcctgcaagtctgctgcaca	8866
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LOCUS	AC003983/c	LOCUS	AC003983	105563 bp	DNA	PRI	13-JAN-1998
DEFINITION		Human PAC	clone DJ0093f03	from Xq23,	complete	sequence.	
ACCESSION		AC003983					
VERSION		AC003983.1		GI:2769694			
KEYWORDS		HTG.					
SOURCE		human.					

REFERENCE	1 (bases 1 to 105563)
AUTHORS	Tin-Mollam, A., Hinds, K., McDonald, R and Ozersky, P.
TITLE	The sequence of H. sapiens PAC clone DJ00933103
JOURNAL	Unpublished (1998)
REFERENCE	2 (bases 1 to 105563)

JOURNAL Submitted (13-JAN-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

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<mailto:sapiens@watson.wustl.edu>

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded or sequenced with an alternate
chemistry; an attempt was made to resolve all sequencing problems,
such as compressions and repeats; all regions were covered by
sequence from more than one subclone; and the assembly was
confirmed by restriction digest.

MAPPING INFORMATION:

This sequence was generated from part of bacterial clone contigs of
human chromosome X, constructed by David Bentley's chromosome X
mapping group at the Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, UK. Further information can be found at
<http://www.sanger.ac.uk/HGP/ChrX>

SOURCE INFORMATION:

This clone was derived from human PAC library RPc1-1, prepared by
Pieter de Jong and coworkers at Roswell Park Cancer Institute,
using the method described by Ioannou et al., Nature Genetics
6:84-9 (1994). The library is from one male donor. For further
details, see <http://bacpac.med.buffalo.edu/>
The clone is available from Genome Systems, Inc.
(<http://www.genomesystems.com>).

VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:

The actual start of this clone is at base position 1 of DJ0093103;
actual end is at 105563 of DJ0093103. The orientation of this clone
is unknown.

This clone contains a single stranded region from 83424-83427.

FEATURES

source
location/Qualifiers

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/db_xref="taxon:9606"

/chromosome="X"

/clone_id="DJ0093103"

/clone_lib="RPc1-1"

/map="Xq23"

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repeat_region

1412..1963

/rpt_family="L2"

repeat_region

3405..3702

/rpt_family="Alu"

repeat_region

3783..4079

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repeat_region

5532..5837

/rpt_family="MER1_type"

repeat_region

5886..6552

/rpt_family="MER1_type"

repeat_region

6553..6848

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repeat_region

6880..7179

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7212..7438

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repeat_region

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repeat_region

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8613..8739

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8746..9410

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9421..9710

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repeat_region

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repeat_region

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repeat_region

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20684..20849

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repeat_region

21732..21912

/rpt_family="MIR"

repeat_region

21913..22236

/rpt_family="L1"

repeat_region

22330..22623

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repeat_region

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23378..23687

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repeat_region

25376..25432

/rpt_family="Alu"

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repeat_region

25730..25951

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31204..31333

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repeat_region

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 Db 50218 TGGACCACTAAAGACAGATAGACTGGCCCCACCAAGTTTGTATTTCTTAAGCA 50159
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 Db 50158 TACATTCAATTTTACTAGAGGAGCATAGAAAGTAAAGAC--AAAACAACTTTAGCAATTA 50101
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OY 7816 tcaatgaatcaatcaggtgtgcaagctgtttagaaatcatcactaaataaaacagtcgaag 7875
Db 47244 TCAACGAATCATACAGTTCAAGCTGTCTTAAAAAATCACTAATTAATAAACGACGAAG 47185
OY 7876 ccttgactatctggcccgcaagaactcagaataagaaatgtatctatctataatagat 7935
Db 47184 CCTTGACTATTCGGCTGTGCAAGAACTCATGATGAAATGCTATCTCAAAATAGAT 47125
OY 7936 tggctctgcactact-ctagcagctgaaagagaggtctcta-aaattacacttaac 7993
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OY 7994 attactgtctacacatagataatcaaaaggaagtagttaaagcgttagttaaagacatag 8053
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OY 8713 cttagaggttgagcccttaaaaggtcagaagtgtgacacacttgacagagctcgatttg 8772
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OY 8773 agacgctagcgtcgatctccagctgtatgaacacactccctcactatcttggt 8832
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repeat_region /rpt_family="Alu" 35603, .35662
BASE COUNT 9620 a 9005 c 9431 g 9083 t
ORIGIN

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Best Local Similarity 75.6%; Pred. No. 0;
Matches 3655; Conservative 0; Mismatches 592; Indels 603; Gaps 34;

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DB 9118 TTCCCTTGTAGGAGAGAGACCCCTTTCGTATTGTTTATATGCTTATCTCAGTA 9177
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QY 2098 -----aggaagaaagtgaataataagcagatagccgcgcgcctagagacagaccg 2152
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DB 9178 TCTGTTTAAAGAAAAACAAGAAAGTAAACCAAGACAGGCGACCTGGCGCAAGCCCA 9237
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QY 2153 aaacagagcctgggagcctgcagcctaagctcgtaagttaaatcgaacccctgaacct 2212
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DB 9238 AAMCAGGCTGGGGCCGCTGCGCTTAACCCAGTAGTTAAAAATCAACCATGACTTAG 9297
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QY 2213 caactgttgtatctatagatccacagacattgtatggaaggcattgtatggaagacat 2272
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DB 9298 AAGCGATGTTATTCATGTTCCAGA-----CATGTATAGAAAGAACAT 9342
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QY 2273 tgggaatctctgttctgttctgttctcaatgtgacacccggtgtcacaagccctgtca 2332
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QY 2333 cgtacccctgggttaactacatcacaccctctcatcgcgcgaaccccttaagatgt 2392
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QY 2393 gaaccccttaaaaggagacaagatgagacatcagacagacgcctggaatttgaagcgtaccc 2452
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DB 9462 GAGACCTTAAAGAGGACAGAAATGTGTCATTCAGGAGATTGGATTTAAGGACAGTACT 9521
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DB 9522 TGCCGATGCTCGACGCTGAATAAAGCC-CYTCTTCTACACTCGGTGTGAAAGTTT 9580
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QY 2513 tgcctcgagctacccgtcacatttctgttccctgacgcggaagcaagcgtatgaac 2572
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DB 9581 TGCTGGGGCTGCTCTGCTACATTTCTTGTTCCCTGAACAGAGACGAGTAACGTAC 9640
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QY 2573 agatggtcgaagcagctcctttaggcggtctttagcctgcctgtggaacatccctgctggg 2632
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DB 9641 GAGCGGCAAGGACGCCCTTGGGTGGCTTAGGCGTCCCTGTGAGCATCCCTGCGGTG 9700
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DB 9701 GACTCTGGCGAGGCTGTGATGACG-CATCCAAAGAGCGCTCCGGGAGGAAATTCGCCG 9759
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QY 2693 ggtgggagacactgcgcagagcagtggtgagcagccccgttgagagatcaacagatgggc 2752
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DB 9760 GGTGGAAAGCCTGCGCAGACAGACACTAGAGCCCCCAGAGGGATTATACACATGGC 9819
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DB 9820 TGAACACTGGGAAGAACTGGCACTTGAGTCCGGACATCTGAACCTTGGTAAGACTAGT 9879
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DB 9880 CTTTGGAACTTGGCCCACTCATCTGAGTGAAGCATGGCCTGATCATCCCATGATGATGCC 9939
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QY 2872 ttatacagcactggtgttggttggttgacttggttgattacttagacaggaacggctgtg 2931
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DB 9940 TGTACTGGCACTTTATTC----- 9959
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DB 9959 ----- 9959

QY 2992 caaggtgaccttccgcgcacttggtttggtttgaactagatgctgtat 3051
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DB 9959 -----TGTATTGACTTGAATTGATGTGAT 9987
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QY 3052 ac-----tttggtttggtttgaactgctgtaattctgaatacctgatttgt 3105
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DB 9988 ACTTGGATTGTTGTTGTTGTTGACCTGGCTGGGTTTGGATACCTC----- 10037
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QY 3106 ttgatttggtttagtgtaactcgcgaagtggtgtgcgtgaccttgaacctgttg 3165
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QY 3166 tttgtgtgtgactgtgtgtgtgagtgatgtgtgtgtgtcgaagaacatggtgcagc 3225
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DB 10087 TTTTGTAGTGCACGTGTGTGTGACGTGTGTGTGTCTCTGAGAGACATGGGTACAGC 10146
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DB 10147 ACAATTAAGCCACCCACACTAGGACATATGTAAAAAATTTTTTCAGAAAGAAAT 10206
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QY 3279 taaggaagattacggtgttactatgaactagaacaaactagaacttgtgtaataaga 3338
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DB 10207 TAAAGGAGATTAGATGTTACTGTGACACAGCAAACTTAGAACT--TGTGAAATAGA 10263
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QY 3339 ctggccaactagaagtggtgtgtgcacatagaagaacccctgaagcttccctgttc 3398
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QY 3399 aatgtatgacacaaggttaacctgttgaagcacaagcacaagaccagtttctgtacgtaga 3458
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QY 3459 caattacagctgtgtttagaacccttcgcgccacagtagttagaagagcgagaagag 3518
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DB 10384 CAGTTACAGCTGTTTGTAGACCCCTTTC--CCCTACAGTAGTTAAGAAAGACAGTACATAGA 10442
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QY 3519 aggaagaagaacaggaagaagtcgaagaagagagagagagagagagaaga 3578
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DB 10443 AGCATTTGCGAGAGGCAAGAAAGACACAGAGAGA----- 10480
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QY 3579 agtcaagaagagaaataatagagaaataatccaagtagttaaagaaataatagtg 3638
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DB 10480 -----AAAAAAGGCATCTATACCAATTCTAAGTTAATTAGACATAAAGCAG--- 10527
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QY 3639 accctattccctttaaagccaaggttaatttaaaccctaaacttgataatgaaggtat 3698
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DB 10527 -----GCTTATTATTATAGCAAAAGATTAATTGAATCCCAACT-----TACAAAGTTT 10574
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QY 3699 tctcgttaacccctgatacaacttaatacaacttgtttagttagtaacaagggctatc 3758
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DB 10575 TCACCAAAAGTGAAAGTTTGCTTAAAAATTAAACAGTAAATGATATGTGTAACCTCTTAA 10634
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QY 3759 ccgaagacactgagcgcttccatacaaaaacttaaccogaagaaacccagatggcca 3818
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DB 10635 TCTTGTGGCTTATAGAGGCTTACTCCAAAGACAAA----- 10671
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QY 3819 gatgcatlcaatctgtagcagcagctgtcttgctaaacaggaacaaacaaagagct 3878
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DB 10671 -----AAAAATTCACTTTAAAAAATAAAG 10696
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DB 10757 ATTAACTGTTGTTTAAAGAAAAAAATGTTGTATAAGTACAGAAAGTGAACATGT 10816
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QY 3996 caaagaattactgcgaagtc---atagaaaaagatgtataaaaaaattatgcacaaa 4052
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Oy	6246	cctgcctcagtcacaaccgggaagctgtagctgctcacgcacgycggaatagaanaact	6305
Db	12847	CCTGCTCCAGTCACACCACCAAGTAGCTGCTGCACGACAGCGCAAGCATAGGAANACT	12906
Oy	6306	catcaggggactcaatttcccttaaatttggactctgttacagtaaggactcaactgacct	6365
Db	12907	CATTGCGGGACTCATTTTCTTTAAATTGGACTTGTACAGTAAGGACTCTCAACGAGACT	12966
Oy	6366	tcccgaactcagaagcagttccccaagtatataactcaafccactgaagtgagacaaagat	6425
Db	12967	TCTTCAGATTGAGNACTGTTTCCAGTATATACATCAAGTCACTAGAGTAGGCAAAA-AT	13025
Oy	6426	tgctacagctccatatattcattgattatgattataagtgtaagagagactctaagaagactg	6485
Db	13026	TGCTACAGTCTCTATTATTATTTAATGTTATTTATAAGTGTACACAGSACTCTAAAGAAACTTG	13085
Oy	6486	tttgtataatgctctctatcccaaggtatgtagccttaggaataataaccaactgctgtg	6545
Db	13086	TTTTGTATAAAT-----CTATTCCAAAGGTATGTATACCCACGGAATTAACCAACTGATGTGTG	13140
Oy	6546	ttatgacccattttaagcccccaatgatacagcttttcttaaataattaagagactgctc	6605
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Oy	6606	ctttcttagtgtagacaagaaglaaagtaagctaaagacagaagaagaagygatccccaagc	6665
Db	13201	CTTTTCTAGAGGACACAGTAAGGTATATACCTAGAACGGAIAAAAAAGAGGGCCCCCAAA	13260
Oy	6666	atgtaaacactaaaatttaagctctgtgcccactlcaatgagcaatggcgatagaataagat	6725
Db	13261	ATGTAACTTAAATTTGGTGCTTTGTGCGCTCTTTATATGTAACAGCATGGAATAAGGAT	13320
Oy	6726	gcgggtctcttaaacgtgaaaaaanaaaagttaaca--cagcaggaanaaataagatatactgcc	6783
Db	13321	GCGGTTCTCTAAATTTGGAAAAAAAANAAGTACACAGTAATAAAAAAATAAGTATCTGTGC	13380
Oy	6784	acgatttaagctctatgycgaatgctgtgtataatctacgtgctgtgtcatctabgactact	6843
Db	13381	AAGATTTGTATTATTATGTG---AAGATGTGTCAAATACGTGCTGTGTCAATTTGGGCTACTT	13437
Oy	6844	agaaaaagatgaaagaagccctgttagc	6873
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RESULT 15			
AP000509			PRI 28-SEP-1999
LOCUS	100000 bp DNA		
DEFINITION	Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region,		
	section 8/20.		
ACCESSION	AF000509		
VERSION	AP000509.1		
KEYWORDS	GI:5926696		
SOURCE	.		
ORGANISM	Homo sapiens DNA.		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
	Eutheria; Primates; Catarrhini; Homiidae; Homo.		
REFERENCE	1 (sites)		
AUTHORS	Shina,S., Tamiya,G., Oka,A. and Inoko,H.		
JOURNAL	Homo sapiens 2,229,818bp genomic DNA of 6p21.3 HLA class I region		
TITLE	Published only in Database (1999) In press		
AUTHORS	2 (bases 1 to 100000)		
REFERENCE	Hirakawa,M., Yamaguchi,H., Imai,K. and Shimada,J.		
JOURNAL	Direct Submission		
TITLE	Submitted (21-SEP-1999) to the DDBJ/EMBL/GenBank databases. Miki		
	Hirakawa, Japan Science and Technology Corporation (JST), Advanced		
	databases Department: 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081,		
	Japan (E-mail:mika@tokyo.jst.go.jp).		

COMMENT	FEATURES	Source
<p>URL: http://www-alls.tokyo.jst.go.jp/, Tel: 01-3-5214-0491, Fax: 01-3-5214-0470)</p> <p>This sequence is conducted by Tokai University as a JST sequencing team.</p> <p>Principal Investigator: Hidetoshi Inoko Ph.D Phone: +81-463-93-1121, Fax: +81-463-94-8884. The sequence is submitted by Human Genome Sequencing in ALLS project of JST</p> <p>Japan Science and Technology Corporation (JST) 5-3, Yonbancyo, Chiyoda-ku, Tokyo, 102-0081 Japan For further information about this sequences, please visit our sequence archive web site (http://www-alls.tokyo.jst.go.jp/HGS/top.html) or send email to webmaster@www-alls.tokyo.jst.go.jp.</p>	<p>Location/Qualifiers</p> <p>1..100000</p> <p>/organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="6" /map="6p21.3" 75817..77730 /gene="POU5F1" /note="match POU5F1 (211899) with account of intervene sequences." /db_xref="GDB:135499" 75817..77750 /gene="POU5F1" 75900..76189 /gene="POU5F1" /note="ORF3:PCR2:The location is between each flanking site of PCR primers." /db_xref="GDB:191806" 77183..77984 /note="ORF3:PCR1:The location is between each flanking site of PCR primers." /db_xref="GDB:191805" complement(99486..99633) /note="W1-15384:The location is between each flanking site of PCR primers." /db_xref="GDB:4580256"</p>	<p>BASE COUNT 26340 a 23491 c 24477 g 25692 t</p> <p>ORIGIN</p>
<p>Query Match 9.6%; Score 2386; DB 10; Length 100000; Best Local Similarity 75.6%; Pred. No. 0; Matches 3695; Conservative 0; Mismatches 590; Indels 605; Gaps 35;</p>	<p>misc.feature</p>	
<p>2047 tcccggtggaaggaagacagaccctcctcatgttttactcagaaa----- 2098</p>		
<p>55293 TTCCCTTTGAGGGAGAGAGACCCCTTTCGTATTTGTTTATATGCTTTTACTCAGTA 55352</p>		
<p>2098 -----aggaagaagaagyaaltaaagacagatagcccgcgactagaacacagaccg 2152</p>		
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<p>2153 aaaccagcgctggcgctgcctgaacctagctcgtagttaaatcagaccctgaacctag 2212</p>		
<p>55413 AAACCAAGCGCTGGGGCTCCTCGGCTTAACCCAGTAGTTAAAAATCAACCATGACTTAG 55472</p>		
<p>2213 caacgtgtgatacctatgatctcagaacatctgtatgaagcgacttgatgaaagagcat 2272</p>		
<p>55473 AACGGGAGTTATTCCTGTTCCAGA-----CATGTGATGAAGAAACAT 55517</p>		
<p>2273 tctgaatctctcgtctcgtctcttcaactgtgacacgcggtgctcacagccctgtgca 2332</p>		
<p>55518 TGTGACACTCCCTGCGCTGTCTGTCTCTCTGACCAACGATGATCAGACCCCTGTCA 55577</p>		
<p>2333 cgtacccctgcttactcaatcgatcacgacccctctcatcggaacccctagaagtgt 2392</p>		
<p>55578 CGTACACCTCGGTACTCAATCAATCAATCAACGACTTTTCATGTGAATCT-TTACTGTGT 55636</p>		
<p>2393 gagcccttaaaaggacagaaagttgagcatcagaagcgtcgatttgagacgtacag 2452</p>		

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QY	2513	tgctcggcgtcactcgtctcaattcttggtctccctgacccgggaagcaagtgattaac	2572
D	55756	TGTCGTGGGGCTCGTCTCTCAATTCTTGTTGTTCCCTGAACAGGAAGCAGGTAATCTGCAC	55815
QY	2573	agatggtcggagcaagctccttaagcggcgtttaagctcgtccctgtgaaactccctcgtg	2632
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QY	2633	gactccaaaccagccagagtgaacgcygactctgagaagctctccctggttagcattgcccc	2692
D	55876	GACTCTGGCCAGCCGTGAAGTGAAGC-GATCCAAAGAGCGCTCCCGGTAGGAATATCCCG	55934
QY	2693	gggtggaaacctcgcacgaagcagtgctgtgcgaagcccccgtggaagatcaaaaggtgac	2752
D	55935	GGTGGAAAGCCTCGGCAAGACAGCAGTACAGCGCCCGGAGAGAGATTAAACACTGGC	55994
QY	2753	tgaacaccgggaagaagaattggcaacttggatgcacccgacacaaactaaacttgtaagaact	2812
D	55995	TGAACACTGGGAAGGAACCTGGCACTTGGAGTCCGACACTTAAACTTGGTAAAGCTAGT	56054
QY	2813	ctttggaactcy-cccactccattttgaagtgaagcattgacctgatacccaagcggtgcc	2871
D	56055	CTTTGGAACTTGCCCACTCCATCTGAAGTGAAGCATGGCGTGAACCCATCCCATGGGTGCC	56114
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D	56115	TGTACTGGCACTTTATTC-----	56134
QY	2932	ggaacttgcacatccatctccatccatctttagtgaagcattgacctgatacc	2991
D	56134	-----	56134
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D	56134	-----TGCTTTGACTTGACTTAAGATTGTGTAT	56162
QY	3052	ac-----tttggttttggttttagccgcgtcttgattcttgaactcgaatttggtt	3105
D	56163	ACTTTGGTTTGGTTTGTTTGCTTGACCTGGCTGGGTTTGGAAATC-----	56212
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Db	56655	-----AAAAAGGCATCTTACCAATTTCTAAGTTATTTTACATTAACAAAG---	56702
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Db	57171	CATAGAGTGTGATTTTACTTACCTTAATTAAGGTTAAAAAATATTGTTTGAAGTG	57230
QY	4227	taagcaagttttaaagttaaigttaaataaaaatctgtgtttaaactaatgaactaa	4286
Db	57231	TAAACAATTTTAAATGTTAATGT- AAAGAAATCTGTGCTAACAATTTACTCTAA	57289
QY	4287	agataaaagagttatcccaagtttcttcgtgaactgtgacattaaagcaaaatgcaacg	4346
Db	57290	AGTTAAAAAGTGTCTCCAGTTTCTGTGACAGTGCACTTAAAGTAAAAAGTGACAG	57349
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Db 59494 GCGGTTCTCTAAATTGGAATAAAAGTACACAGTAAATAAATAGTGTATCTGTC 59553
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 Job time: 118599 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 28, 2000, 11:15:29 ; Search time 20117.6 Seconds

(without alignments)
-3018.640 Million cell updates/sec

Title: US-09-339-352-7_COPY_1_20000

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Scoring table: IDENTITY_NUC

Searched: 821193 seqs, -1518192014 residues

Database: GenEmbl.*

Word size: 0

Number of hits that pass the threshold: 1642386

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50: gb_pl3.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20000	100.0	102258	11	HS295C6	297876 Human DNA s
2	5877.2	29.4	128230	11	HS31314	299943 Human DNA s
3	1744	8.7	7728	11	AF058907	297876 Human DNA s
4	1701	8.5	135305	11	HS71113D6	297876 Human DNA s
5	1646.8	8.2	137413	42	AC011036	297876 Human DNA s
6	1611.8	8.1	138088	43	AC010877	297876 Human DNA s
7	1586.6	7.9	158463	44	AC011019	297876 Human DNA s
8	1560.8	7.8	227567	42	AC008554	297876 Human DNA s
9	1517.8	7.6	226345	40	AC005406	297876 Human DNA s
10	1442.6	7.2	36921	40	AC004185	297876 Human DNA s
11	1442.6	7.2	37139	40	AC006047	297876 Human DNA s
12	1430.2	7.2	100000	10	AP000509	297876 Human DNA s
13	1430.2	7.2	236822	10	D84394	297876 Human DNA s
14	1392.6	6.9	97906	32	HS1141E20	297876 Human DNA s
15	1381.8	6.9	79376	11	HS45466	297876 Human DNA s
16	1341.4	6.7	174768	41	AC009330	297876 Human DNA s
17	1339.2	6.7	161428	41	AC009542	297876 Human DNA s
18	1337	6.7	182011	33	AC007683	297876 Human DNA s
19	1331.2	6.7	191235	42	AC012487	297876 Human DNA s
20	1250.2	6.3	105563	11	AC003983	297876 Human DNA s
21	1230.6	6.1	163738	42	AC009505	297876 Human DNA s
22	1100.4	5.5	200607	44	AC016775	297876 Human DNA s
23	1082.8	5.4	173157	42	AC011895	297876 Human DNA s
24	1081.2	5.4	203488	42	AC009468	297876 Human DNA s
25	1020.4	5.1	129480	41	AC008428	297876 Human DNA s
26	961.4	4.8	110409	42	AC010487	297876 Human DNA s
27	914.2	4.6	268399	33	AC004469	297876 Human DNA s
28	901.4	4.5	144304	32	HS0383P5	297876 Human DNA s
29	882.2	4.4	123585	11	AC004707	297876 Human DNA s
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31	867.6	4.3	122000	11	AC003093	297876 Human DNA s
32	837.4	4.2	59380	42	AC010521	297876 Human DNA s
33	836.2	4.2	118226	11	HS46618	297876 Human DNA s
34	834.6	4.2	158810	44	AC011604	297876 Human DNA s
35	819.2	4.1	142552	11	HS581B8	297876 Human DNA s
36	818.4	4.1	76540	11	AC003678	297876 Human DNA s
37	815.2	4.1	137693	40	AC003689	297876 Human DNA s
38	812	4.1	149876	32	AP000437	297876 Human DNA s
39	812	4.1	131922	32	AP000589	297876 Human DNA s
40	809.6	4.0	151600	43	AC011682	297876 Human DNA s
41	793.6	4.0	171636	10	HS215K18	297876 Human DNA s
42	792.8	4.0	192334	40	AC007319	297876 Human DNA s
43	781.8	3.9	132805	11	HS339A18	297876 Human DNA s
44	774	3.9	214717	44	AC016759	297876 Human DNA s
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ALIGNMENTS

RESULT 1
HS295C6
LOCUS HS295C6 102258 bp DNA PRI 23-NOV-1999
DEFINITION Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains
ESTs, CA repeat, SRS and Cpg island.
ACCESSION 297876
VERSION 297876.1 GI:2582745
KEYWORDS 1q24; Cpg island; repeat polymorphism.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 102258)
AUTHORS Grafham,D.
TITLE Direct Submission
JOURNAL Submitted (27-OCT-1997) Chromosome 1 Project Group
(http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Nov 2, 1997 this sequence version replaced gi:2465042.
IMPORTANT: This sequence is the entire insert of clone 295C6.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variations annotated may not be found in the sequence submission
corresponding to the overlapping clone as we submit sequences with
only a small overlap as described above.
This sequence was generated from part of bacterial clone contigs of
human chromosome 1 constructed by the Sanger Centre chromosome 1
mapping group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1/
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key
The true left end of clone 295C6 is at 1 in this sequence. The true
right end of clone 295C6 is at 102258.
295C6 is from the library RPCII constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/
Location/Qualifiers
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2028..2310
/note="AluSg repeat: matches 300. .1 of consensus"
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223618"
4766..4897
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5146..5448
/note="AluJo repeat: matches 302. .1 of consensus"
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5503..5795
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repeat_region
5797..5925
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5923..6039
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6123..6415
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9002..9302
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15702..16064
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similar to endogenous retrovirus POL POLYPROTEIN"
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26022..26312
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26752..27050
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repeat_region
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28316..29066
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29517..29629
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29631..29928
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29937..30237
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repeat_region
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repeat_region
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35744..36466
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36692..36944
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36999..37299
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37924..38114
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repeat_region	38958..39380 /note="L1M3 repeat: matches 699..85 of consensus"
repeat_region	39385..39875 /note="Alusg repeat: matches 292..1 of consensus"
repeat_region	39877..39951 /note="L1M9 repeat: matches 88..14 of consensus"
repeat_region	39944..40019 /note="L1 repeat: matches 4416..5390 of consensus"
repeat_region	40769..41662 /note="L1PA2 repeat: matches 1..893 of consensus"
repeat_region	41764..42556 /note="L1 repeat: matches 5133..4305 of consensus"
repeat_region	42557..42557 /note="Alu repeat: matches 1..301 of consensus"
repeat_region	42876..43325 /note="L1 repeat: matches 4313..3215 of consensus"
repeat_region	44235..44498 /note="MER3 repeat: matches 3..272 of consensus"
repeat_region	44788..44660 /note="MIR repeat: matches 154..82 of consensus"
repeat_region	44933..45220 /note="Alusg repeat: matches 289..2 of consensus"
unsure	45304..45336 45337..45537
repeat_region	/note="Alu repeat: matches 1..301 of consensus"
repeat_region	45934..46220 /note="Alub repeat: matches 302..14 of consensus"
repeat_region	46817..46935 /note="MIR repeat: matches 35..154 of consensus"
repeat_region	47393..47677 /note="Alus repeat: matches 1..302 of consensus"
repeat_region	48309..48404 /note="MIR repeat: matches 48..140 of consensus"
repeat_region	48620..48662 /note="MER1 repeat: matches 347..102 of consensus"
repeat_region	48865..49159 /note="Alus repeat: matches 1..296 of consensus"
repeat_region	51182..51467

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Matches 20000; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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Db	181	TTTGGTGGGAAAGCTCATATGCTATCCACGCTGGATCAAGAGATTTCGCGAGTAGAAGTC	240
Oy	241	cacacagtagaanaactgattatatacttatacctaatactcgtatattaatagagcag	300
Db	241	CACACAGTAGAANAACCTAGTATTTATCTTTATCTTAATATATGCTGTATTAATATAGAGCAG	300
Oy	301	gttgaaacaacatctcgtcttaagttcttgttgcagaanaactcagccaagtactaa	360
Db	301	GTGGAACAACCATCTCTGCTCTTAACAATTTTGTGTGCAGAAAACTCAGCCACACTAAGTCAA	360

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Db	361	AGAAATATTGTTTAGTACCTTAATTTGGAGTAGCATTGTGCGGAGTACCTAAAGATG	420
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Db	421	CAGGCTTAGGCGCTTAGAAGACACACAGCACAATACCTGTGACAAATTAAGATCTATTTC	480
OY	481	atggtgttcctgaatttggctaaagtgtgacaagtgtgtgtgaggagaggaagacatt	540
Db	481	ATGGTGTCTGATTGTTGGCTAAAGTGTGACAAAGTGTGTGACGAGAGAGAGACATT	540
OY	541	gtaatacctattgtcaagaagagcagcgccctgcattccctgtgcttttgaattcccca	600
Db	541	GTAATCACTATTGTGCAGAGGAGCGCCCTGCCATTCTGTGCTTTTGTGACTTCACA	600
OY	601	gctgtccctttgtatctctctctgtgcctcccttctccagaagaatccggtttctc	660
Db	601	GCTGTCTCTTTGTATCTCTCTCTGTGCTCCCTCTTCTCCAGAAATCCCGGTTTCTC	660
OY	661	ctatactgccccagaanaattatgtatctcatagacatacatatcatctcgtgtcatalga	720
Db	661	TCTATCTGCCCTAGAAATTAATTAATTTCTCATTAATGACATATATATCTGTGTCATAGA	720
OY	721	ccaagtgtcagaagattcacagctctcatcccaactttcaatcctaagcttgaatacggt	780
Db	721	CCAAGTGTCAAGAGATTCAACAGCTCTCATCCCAACTTTTCACTTAAGCTTGAAATTCGGT	780
OY	781	agctaatgtgacttctctgtgacattttggccaggaatgtccctctgttgaaggacaaattag	840
Db	781	AGCTAATGTGACTTCTCTGTGACATTTTGGACAGAGATGCTCTCTGTGTAGGACAAATTAG	840
OY	841	aattctcaacttgcacaaaaaacagtagaanaatagcttagtccatccctctttttt	900
Db	841	AATTCTCAACTTGCCTCCAAAAACACAGTAGAATCTAAGCTATAGCTATCTCTTTT	900
OY	901	ttttgagaatgtagtctactcttgttgcacaaagctgtgagtgcagatggtctgacatcgct	960
Db	901	TTTTGAGATGGAGTCTCACTCTTGTGCCCAAGCTGAGTAGCAATGGCTGATCGGCT	960
OY	961	cactgcaacctgcgctctcgtgtgtcaagaagattctctgcctcagcctcttgagtagct	1020
Db	961	CACCTCAACCTCGCGCTCTGTGGTTCAAGAAATCTCTGCTCGCTCTGTGAATACT	1020
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Db	1021	GGGATTATAGGACCCACCCACCAATGCCCGGCTAATTTTGTGTTTGAAGAGACATGGG	1080
OY	1081	atttaccatgtgtgacagcagctgtgtctgaaactcctgacctcaggttgaatccacctgctc	1140
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OY	1141	ggcctcccaagtgctgggattaaeagtgtagtactgtgctcttcatatagtagaacac	1200
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OY	1261	caactttctaacaacttgaagaattgctttaagatgtgacatgaattggagcttgaattacat	1320
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Db	1321	AAAACATTCCTGAAGATCATTTTCTTTAAAGAAATATATATCATCTTCTTCTTTC	1380
OY	1381	ttttctttctttttgagacagagttttctcttgttgcagagccgagaggtgacatggcgt	1440
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OY 9241 catctcactcagccttggcgaatgagagcgaaactagtcttaaaaaaacaacaaca 9300
DB 9241 CATTCACCTCCAGCCTGGCAATGAGAGGAACTAGGCTTAAAAAACAACAAAACA 9300
OY 9301 aacaaacaacaacaacaacaagaagaagaccgagagagagatcactgaagaagctcag 9360
DB 9301 AACAAACAAACAAACAAACAAACAAACAAACCCAGAGAGAACTACTGAAGACTCAG 9360
OY 9361 agagcactcacagtgagtcagcttccacatctgcataagacagagacaacaatacca 9420
DB 9361 AGAGCACTCACAGTGAGTCAAGCTTCCACATCTGCCATAGACAGAGAACCAATACCA 9420
OY 9421 gacacacacattgccagcaggttaagacctgtcttaagtgcaggtcattgtttaaagc 9480
DB 9421 GACCAACACATTGCCAGCGAGGTAAAGACTTCTTAGTGCGAGTCAATGTTTAAAGC 9480
OY 9481 ttaccagtttgccttctcctgtcacttgcacataagaatgctttagtcaactgagttaa 9540
DB 9481 TTACCAAGTTGCTTCTTCTGTACTTGTCCATTAACAAATGCTTTAGTCACTGAGTTAA 9540
OY 9541 agtgagatataccatcccccatatgatgaagaagaatagagcttcttcaatgaagcaat 9600
DB 9541 AGTGAGTATACCCATTAACCCCATGATGAAGGAATATAGACTTTTCTCTAAGCAAGT 9600
OY 9601 ttaagaagcgtaacagagagcaacatggaagaagtgaacacatcactccaagc 9660
DB 9601 TTAAGAAGCGCTAACAGAGGAGCAACATGGAAGGTGCAACATCACTCTTACCAAGC 9660
OY 9661 attatgaatggtctccttcaaaaggtgagacagacaaatggtgtgctcacaacctgta 9720
DB 9661 ATTATGAATGCTCCTTCTTCAAAAGGTGAGCACCAAGATGTTGCTCACCTGTAAAT 9720
OY 9721 cccaagcatttggagagctgagatggagatgtctttagcccaagagttctatgac 9780
DB 9721 CCCAGCATTTTGGAGGCGTGAATGGAAGATGTTGTTGAGCCAGAGATCATGATCAGC 9780
OY 9781 ctgggcaacactgtgagaccatctctacagaataaanaattaccggaggtgtcaac 9840
DB 9781 CTGGGCAACACTGTGAGACCCCATCTTACAGAAATTAATAATTTTCCGGAGGTGCACAC 9840
OY 9841 ctgtagttcgttactcagaagaagcggagcgagagatggtgttggccccagagaggtcaa 9900
DB 9841 CTGTAGTTCTGTACTCAGAAAGCTGAGGCAAGAGATGCTTGAAGCCAGAGAGGTCAAG 9900
OY 9901 gctgcagtgagccatgagacacacactcagcctgagctgtgacagatgaagacctg 9960
DB 9901 GCTGCAGTGAGCATGATGAGCAGCACTACCTTACGCTGGGTGACAGATGAAGCCCTG 9960
OY 9961 tctcaaaaagaaaacagaaaagaaaagaaaatttctttaaaggttgggccaagaag 10020
DB 9961 TCTCAAAAAGAAAACAGAAAAGAAAAGAAAATTTTAAAGAGTGGGCGCAAGAAAG 10020
OY 10021 atactgaatagggacatcaagaacacatactaagaatctgttgaagcttagaccgagag 10080
DB 10021 ATACTGAATAGGACATCAACACATCACTAAGAAATCTGTAGAGTCTTAACCGAGAGG 10080
OY 10081 aatgtatgcagatgtcagagagtcagaaatagaagaagttactttagctcaggtctt 10140
DB 10081 AATGTATGCAATGTCTGAGAGTTCAGAAATAGAAAGGTACTTACAGTCCAGTCTTT 10140
OY 10141 ggaagatgcagctacatgtgaagttcaagaacagatcttgttggagatgtctgaagctgac 10200
DB 10141 GGAGATGCAGCTCACATGTGAGGTCAAGACAGATCTTGTGGAGATGCTGTAGCTGTAC 10200
OY 10201 tgcacaatatgaanaagtgtgtgttctcgttcttcttcttcttcttcttcttcttcttct 10260
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Db	10201	TCGACCAATGACATATTAGGTGGTGTTCCTTCTTTATTTACGGCCCTGGACCTCTCA	10260
Qy	10261	gggaaatgtaaaggaaggaacacagggacaaatgaatgaagaatgcggataag	10320
Db	10261	GGGAATGTTAACGAAGGACACAGGACATTAATGATGAAGATGAGAGTCCGGATTAAG	10320
Qy	10321	cttctccataaactctccagaggtgtaatcccaaaactgsgctctcaatgataaaat	10380
Db	10321	CTTCTCCATAAATCTCCAGAGGTGCAATCCAAACTGGGCTCTCAATGTATTAATAAT	10380
Qy	10381	aatccttctctcttcaactctcgaacaagtgcagaagaagagaacacccaatag	10440
Db	10381	AATCCTTCTCTCTTCTCACTATCGACAAGATGCAGAAAGAGAAGAAACCCATAG	10440
Qy	10441	agctcaggtttttttacacatgtaatggtatgcatatgtaaccattgagcttccgttt	10500
Db	10441	AGCTCAGGTTTTTTTACATGATGGGATGCAATGATGATTCATTGAGCTTCTGGTTT	10500
Qy	10501	gcttaatgtagcagcgaagaagaactcaatcttcttccagtaacttgcattcat	10560
Db	10501	GCTTATGATGACACGGAAGACATACTCAATTTCTTTCCAGTAACCTTTCATCTCAT	10560
Qy	10561	ttaataatcaatgaactgaatattgtgctbatttgacaagagctggtcggaaatgaaact	10620
Db	10561	TTAATATTCATTAACTTAGAATTTGTGGCTATTGTGACAGAGCTGGCTGGAAATGAGACT	10620
Qy	10621	tacttgtaaaagcttgtaagaatgtaagcaatttgagaaatagatggaatttaag	10680
Db	10621	TACTTGCTCAAAAGCTTTGTGTAAAGATAGTGCAAATTTGGAGATATGATGAGACTTTAAG	10680
Qy	10681	ggtaccaccaaaaagctaaactgaagtgtcccaatcaataaaataactggtttgttaattat	10740
Db	10681	GGTACCCACAAAAGCTAACTGAAGTCCCATTCATTAATAAAATPACTGGTTGTATATAT	10740
Qy	10741	gagtcattttaatctatgtgaacataacagtttcctcgggggaaatcctacttgaattatt	10800
Db	10741	GAGTCATTTTAACTATTTGAACATATACAGTGTCTGGGGAATTCATCTGAATTTATAT	10800
Qy	10801	caaccagcatalataatcaagcaatgcttactgagcaccctcggctgaagtgcgaacaa	10860
Db	10801	CAACAGCATATATTAGCACAATGCTTACTGAGCACCCCTGGGCTAGGTGCTGAACAAA	10860
Qy	10861	actagtcctgcgcctgcgagcagcgaatgctattctagcttgaatgtggtatgtgtgc	10920
Db	10861	ACTAGTCCTGCCTCTGCGCAGCCGATGCTATTCAGCTTGAAATGTGTATGTGTGC	10920
Qy	10921	acttaaaaaaagaatacagagtccttctctcaataagactcccccctaagtgtct	10980
Db	10921	ACTTAAAAAAGCATATACAGTCCCTTTTCTCATATAGACTACCTCCCTATAGTAGTCT	10980
Qy	10981	gaattattatcactcatlaagacatttatgtgcatacacaaggttcaggtgtcttct	11040
Db	10981	GAATTTTATTCACACTCATTTAAGCATTTTATTTGATGATCATGAGGTGAGCTGTCT	11040
Qy	11041	aggtactgggaataacagtttcaaaaataacggagcccaatttaagtgtaaccactt	11100
Db	11041	AGGTACTGGGAATACAGTCTCAAAACAAATACGGAGCTTATTTAGGCTCAACACACTT	11100
Qy	11101	acgtagcaggtcctgccttcaacacatgtgtaaggtgcacaatgcagaanaacggctcccc	11160
Db	11101	ACGTACAGAGCTCTGCTTACACACTGTGTAAGGTGCACAAATGCAANAACCGGCTCCCC	11160
Qy	11161	agttctactgctccagactgctaagtgtgcttlttcttccctctgagaagaatgta	11220
Db	11161	AGTTCTCACTGCTCCAGACTGTCTAAATGCTGCTTTTGTTCCTCTGAGAAGAGATTGA	11220
Qy	11221	gttaaccacatctcttctcttctgtctgtaagcagtcataataaagtgtataaactgctgt	11280
Db	11221	GTTAACCCATTCTTCTCTTGTGTGCTTGACAGTCAATTATTAAGTGTATTAACCTGCTTGG	11280
Qy	11281	ttaacacatacctaagtctactctctgcagcccggttctgtcaaccaatacttagcccttt	11340
Db	11281	TTTCAACATACCTAAGTCTACTCTCTGCAAGCCCGGTTCTGTACCAAAATCTTAGCCCTT	11340
Qy	11341	gactagcccttgaaacaglttaattaatgaaaggtlaagcactacatactgttttgagtttg	11400
Db	11341	GACTAGCCCTTGAAACAGTGTATTTAATGAGAGGTAAAGCACTACATTTGTTGAGTTTG	11400
Qy	11401	actggtatctttaaaaagaatggggaggtatagaatttaagtttaactcttgatagcct	11460
Db	11401	ACTGGTATCTTTAAAAGATGGGGAGATAGAAATTTAAGTTTAACTTTGGGATAGCCT	11460
Qy	11461	tgtaataatattatcatalaataatltgaagaataaagcaggaaacaaaatactgaattca	11520
Db	11461	TGTTATGATATTTATTCATTAATTTGAAGAAATPAAGCAGGAACAAATAATCATGAATCA	11520
Qy	11521	ataataaaaacatltgctcgtgttcttcttcaatcaataatgagagattggttcttttaag	11580
Db	11521	ATATATPAACATTTGGCTGGTTTCTCTTAATCTTAATTAATGAGATTGGGTCTCTTTTAAAG	11580
Qy	11581	tgaaaaaaagccaacactacatacttacttactatgtgtccaaagtactcggagatgctct	11640
Db	11581	TGAAAAAAGCCAACACTTACTATCTATTAATGATGATGTTCCAAAGTCTCGGGATGCTCTT	11640
Qy	11641	tacataaataactcaacttaatccctcaacaatccataaaagtgtactatgtgaactcat	11700
Db	11641	TACATATATTAACCTCACTTAATCTCACAACAATCAATTAATTAAGTGTACTATTGAATCTAT	11700
Qy	11701	ttgcgtgaaaaatttgggcagcagaagaatttaagttaacttgcacaggtgcacagaatagt	11760
Db	11701	TTCGTGAGAAATTTGGGCACAGAAAGATTAAGTAACTTGGCCAGGTCACACANATAGT	11760
Qy	11761	taaigtgccaaaagacttgtcagtaacataatcaacacagctttggttagcagtttccaaac	11820
Db	11761	TAAITGTCCTCAAAAGCTTTGCACTATCATATATCAACACAGCTTTGGTACAGTTTCCAAC	11820
Qy	11821	aagattctgcttcaagcacacaactggaagaattttaacaaaagcaaacactcaaacagct	11880
Db	11821	AAGATTCTGCTTCAAGCCCACTCAAGTAAAGTTTAAACAAAAGCAAAACATCAACAGGT	11880
Qy	11881	tccttagccccaatccacatacctactcttlltaacttlltagagttlaagaatcacaatccat	11940
Db	11881	TCTTAGGCCCAATCCACATCCACTCTTTTATCTTTTGAAGTTAAGTCAACATAATTCAT	11940
Qy	11941	atttttaagaagactctcttgaataactctgtgaatgcgaacagctcaagccctgacattta	12000
Db	11941	ATTTTAAAGAGCTTCTTGTAAATCTTGATGATCCAAACAGTCTTAACCCCTGCACACTTA	12000
Qy	12001	gaactactgatatgttcttgcctctgacccgaagttaacaaagaagaagactgtaattata	12060
Db	12001	GAAACTACTGATATTGTCTTGGCTATGACCTGAAGTACAAAAAGAAAGCTGTATTATA	12060
Qy	12061	aataataatacattgcacacaaacttatalcgaatcatttlatgtacaattatgaagcaca	12120
Db	12061	AATATATATCAATGCACCAACTTTATTCGATCATTTATTAATGTCAATTTAGAGGCACA	12120
Qy	12121	tttctcatcacaatg	

Oy	12421	ttgcaatccagccctggcgacagacgagactctgtctcaaaaaaaaaaaaaaaaa	12480
Db	12421	TTGCACTCCAGCCTTGGGGACGAGACGAGACTCTGTCTCAAAAAAAAAAAAAA	12480
Oy	12481	aaagaagctcaagcttccctgaaggagagaaacagatatataagtaatatgcca	12540
Db	12481	AAAAAGGCTCAGATTTCTCTGAGGAGAGAAAAAGATATATAGTAAATGGCA	12540
Oy	12541	tatgcctaaatagatagagtgtaagataaaactgaagatggtgtccaaagcttcagaa	12600
Db	12541	TATGCCATATATGATPAGAGTATATAGTATACATGAAATGTGTTCCAGCCTTACAGAA	12600
Oy	12601	gccttggtgaagaagaatagatcagtcagtcagatcctggggaagcttcaccaaagagt	12660
Db	12601	GCCCTGTGAGAGAAATAGTCATGTCTAGTGAATCTGGGAAGTTCTCACAAAGAGT	12660
Oy	12661	gacattgaagaatgagcaacatctctaggttaaaaaaaacctttggtcttatcta	12720
Db	12661	GACATTGAAAGATGAGCACCATTTCTCAGGTAAAAAAAATCTTTGGCTTTATCTTA	12720
Oy	12721	ttaccacgggaagctattttcgagagataaaatagtggttggttgatattgatatacc	12780
Db	12721	TTACCACTGGGACTTATTTCCGAGATATPAAATATAGGTTGGTGTGATTTGCATATACC	12780
Oy	12781	tgaagattatatgaagaagtgaaatlaaagcagaaggtgtgaagcagaagttcttgaa	12840
Db	12781	TGAGAAATTATPAGAGATGAAATGAAGAGAGAGGTGAAGCACAGAGTTTGTGAA	12840
Oy	12841	agctatggaataagtcceagaaaaatgaataagagcctgaacctgccaatgagaagga	12900
Db	12841	AGCTATGGAATATAGTCCAGGAAAAATGATTAAGACCTCGAATATAGGCATATGGAAGGA	12900
Oy	12901	ggaacagaagagatctccagaagacctgaggtaaataagtaagaacctggcaatgaataatcg	12960
Db	12901	GGACAGAGAGATTCGACGAGACTGAGGTTAAAAATAGTAGACTTGGCAGTGAATTAATGCG	12960
Oy	12961	ggaatgtggcaaaaaaagaaggcaaggaataacttaaatgatatacagaatgagataatlg	13020
Db	12961	GGAATGTGGCAAAAAAAGAGCAAGGATAACTTTAAATGATACGAATGGCATATTTG	13020
Oy	13021	ctactcaatgaaatcaaggaatacaggttcagagatgaggaagaagaaggcactatagtataaaa	13080
Db	13021	CTACTCAATGAAATCAAGGATCAGGATCAGGAGAGGAAGAAAGGGCACTATATGTAATAAA	13080
Oy	13081	atgaatctggcaatgaacactcaactcagcgtagtcaactacaatccaatggaatatata	13140
Db	13081	ATGAATTTGGCATTGACACTCACTCAACGCGGAGATCACTACATCCAAATGGAATATATA	13140
Oy	13141	caaggctcttagaaatagttgttggtgttataaagaaggtgtyggagctgaaataaaat	13200
Db	13141	CAAGGCTCTTAGGAATATGTTGTGTGTTTATAGAGAGGTGGGACTGAATAATTAAT	13200
Oy	13201	ttgtgtatccaatatatagcagacagtcgtgatataatctcggggagaagctaaactgttg	13260
Db	13201	TTGGTGATCAATATATATACAGACACTCGATATTACTGGGAGACGCTAAACCTTGTTG	13260
Oy	13261	agtgcttcttaagaagaacactgtttctaagtggttcaactacaactagtcattaa	13320
Db	13261	AGTGTTCTTATGAAGAAGACACTGTCTTAAGTGTTTACTACTATATATCTAGTCAATTAA	13320
Oy	13321	actcatcccaagtgcagtcagctactatatttccctccattgataagataaagcag	13380
Db	13321	ACTTCATCCCAAGTAGCTAGCTACTATTATTTTCTCCATTGATGATGATAAGCAG	13380
Oy	13381	aaacataaaggaggaatcactcgtctgaagttgtctcaggttagcaagtgataaggccctggg	13440
Db	13381	AAACATTAAGAGGGATPACTCACTGCTTAGAGTTGCTCAGGTAGCAAGTGAATPAGGCTGGG	13440
Oy	13441	ggttcaaaaccccaatgagctcagacagaagccttgatattgtaaccaattgtaacat	13500
Db	13441	GTTCAAAACCTTAGTGGTGTGCGACAGAGGCTGCATATATGTAACCACTTTGGTAACTTAT	13500

QY	13501	atctcaacaagaatgaaaaaatgagctgcagagagagccagactctcaggagtaatctc	13500
Db	13501	ATCTCAACAAGAAAGAAAAATGAGTGTCTGAGAGAGCCAGACTCTTAGAGGTAAATGTT	13500
QY	13561	aaggagacctttcaaggcatcctaattctcaacagaccttttgtttaggtttgaag	13620
Db	13561	AAGGAGACTCTTTTCAAGGACATCTAAATTTCTTAACAGACCTTTTGCTTAGAGTTTGAAGG	13620
QY	13621	atgaggaggagaatgaagcaacttaggaacaagaagcctcacatcccttaagaagcctctgca	13680
Db	13621	ATGGAGAGGAATGAAGCACTTAGAGCAAAAGCCTTCACATCCTTAAAAAGCCTCTTGCCA	13680
QY	13681	atgtagctgaacacctcccaaacaccctggctcttgtagatctggccgaattctctccc	13740
Db	13681	ATGTGTGCTGAACTCCTCAACACACTGGCTTGTGGTGATTTGCCAGTTTCTTCCCC	13740
QY	13741	ctactcttgaccacagatgctcttcaagcttaagaatctcaataatctca	13800
Db	13741	CTACTCTTGTAGCCACAGATGCTCTTACCAGCTTCAATCTTCTAATAACATATTTTCCA	13800
QY	13801	atgtgtttgctctttcaagagtgccacacccctggaaatcccgagaataatgaagaaactgta	13860
Db	13801	ATGTGTTTTGCTTTTCAAGTGGTCCATCTCTGGAATCTCCGAGAAATTAAGGAATCTTA	13860
QY	13861	caaaagaatcatgaataatcgata.tgggaaataatgacaagggaaacta.ctgctatgcaa	13920
Db	13861	CAAAAGAATTAATGAAATTAATGAGTATGGGAAATATGCAAAAGGAATCTGTGCTATGCA	13920
QY	13921	ctttgggcaaaacacttaactatctctgtgctttaaatectca.tg.tgttagataagtgct	13980
Db	13921	CTTTGGGCAAAACACTTAACATTTGTGTCTTAAATCCCATCTGTAGTAATGTGT	13980
QY	13981	cccaaccccttttggcaccagagagcaagtcttttggaaaaacaattcttcagaagctggg	14040
Db	13981	CCCAACCTTTTGGCACCAGAGCAAGTACTTTGTGTGAAAAACAATTTTTCATGAACTGCGGG	14040
QY	14041	cagaaggaggatga.ttttagagatgatc.aagtgcatcata.tttat.tg.tgcaact.tgcttcta	14100
Db	14041	CAGAGGGAGTATTTTAGAGATGATTCAGGTGCATTAATTAATTTAGTCACCTTGGCTTCTA	14100
QY	14101	ttattacatttgaatatataatgatgaataataatacaactcaacataatg.ttgtatgaatc	14160
Db	14101	TTATTACATTTGAAATATTAATGAATATTAATAACATCACCAATTAATGTAGATGAATC	14160
QY	14161	agttggagcccttgaagcttg.tttcccttggaaactaga.ttg.tcccatct.tggagg.tg.atgag	14220
Db	14161	AGTGGAGCCCTGAGACTTGTTCTTTCGCACTAGATGCTCCATCTGAGGGTGAAGAG	14220
QY	14221	ccagtgacagatcatc.aagcat.tagatctc.ataa.gagca.tg.caa.cct.tlag.tccct.tgc	14280
Db	14221	CCAGTGACAGATCATCAGGCACTTAGATCTCATATAGAGAGATGCMACTTAGTCCCTTGC	14280
QY	14281	atgcacaa.ttcaacaat.taa.gtt.ttcagg.tccctat.tgaa.tcaat.tgct.tgct.tgcatc.tga	14340
Db	14281	ATGCACAATTCACAAATAGGTTCAAGGCTCCATATGAAATCAATATCTCTCTGTATTCGA	14340
QY	14341	caagggaggagcct.taa.g.tg.taa.tg.tga.aat.tg.aag.tg.gagctataat.taga.gat.aa	14400
Db	14341	CAAGGAGAGAGACTTAGTGTGAATGTAACGAATGGGAGTGGCATTAATATAGAGATCAA	14400
QY	14401	gcttcaact.tgct.cacc.aac.tg.tgct.cctc.tgct.tg.tg.tgct.tg.tg.ttc.aa.cagg.ccat	14460
Db	14401	GCTTCACTTGTGCACCCACTGGTGGCTCTCGTGCTGTGCTGTGTTCTTAACAGGCGCAT	14460
QY	14461	gaactagatca.ccaagg.tgt.tgga.gaa.cccct.tg.tg.tgataat.ttc.aag.aa.aag.cagg.gcca	14520
Db	14461	GAACTAGTACCAAGGGGTTGAGAACCCCTGTGTAGATTAATTCAGAAAAAGACAGGGCCA	14520
QY	14521	gtctcact.tgcatcaact.tg.taa.gaa.aag.tg.aat.tg.tg.tcc.aag.tg.tgct.tgata	14580
Db	14521	GTCCTCACTGGCATCTGTTATGAGAACAGAGTGACTTTGTGTCCAGAGTACGCTTAGATTA	14580
QY	14581	gctatga.taga.aagg.taa.gaa.aa.aat.tag.tc.aag.caga.tg.gca.ttg.tg.at.ttc.ttg	14640

Db	14581	GCTATGATAGAAAGGTAAACAAAAAATTATAGTACAGATGGCCATTGTGGATTTCCTAG	14640
Qy	14641	tatgatattccaagaataccctaataatgtaacgaatgttgaatcattccagagaagatt	14700
Db	14641	TATGATATTTCGAAGTACCTCTAAATATGCAAGAAATGTTGATGCACATCCAGAGATT	14700
Qy	14701	gggaagcaattctaccacatcggtactgcgaatatacaagccaaagaatgtcaatc	14760
Db	14701	GGGAGCCATTATCTCAACATCTGGATACGAGATATACAGCCAAAGAGATGCTAAATC	14760
Qy	14761	acaatgcaccagaagaagatctgctgcctgcacatggtctatgttcgagaagtaata	14820
Db	14761	ACAATGCACCAAGAGAGAGTCTGTGCTGCCATGGGTATTGTGCAGAAATATAFA	14820
Qy	14821	ctagctagttaccctgaaacaatggaaaatgtcatlaagaagaacagtagaaccttccaa	14880
Db	14821	CTAGCTAGTTACTCTCAACATGTGAAAAATGCATTAAGAAAGACGTGAACCTTTCTCCAA	14880
Qy	14881	cagttcatagacttatcttcgaaggtttgctgctgtctcttaataatgtttacaagtctc	14940
Db	14881	CAGTGTCAATGACTTTATTTTCGAAGTGTGCTGTGCTGTTTATATATGTTTACAAGTCTC	14940
Qy	14941	taggcctcaggacattgycgatbaaacatctgaaatggatagaagtttgaatgaagctgat	15000
Db	14941	TAGGCCTCAGACATTTGGCCATGACATCGATGGATATGAAGATTTGATGGAAGCTGAT	15000
Qy	15001	cttatccaatgaaatgycgaataatccctgttttctgagaataatcaagaacagaagaagtc	15060
Db	15001	CTTATTCATGAAATGGCCATATATCTGTTTGTGAAAAATCMAAACAAGAGAGATT	15060
Qy	15061	tttaaatatatacttttgaanaataagagttgaagaagaacctgctctctccatctc	15120
Db	15061	TTTAAATATATTTTTTGAAATTAATAGAGTTGAAGGAACCTGTGCTTCTCATATTC	15120
Qy	15121	agcetaaatatgtagagattctccaagctacatcgcgaatggtcttlatgctgctctga	15180
Db	15121	AGCTATTAATGAAGAGATTTCCTCAAGCATATCCGCAATGAGTTCTTATTTGGCTTCGA	15180
Qy	15181	tatctccctctctccctgtcttcgaagccgtatatttaacatcagataatctctct	15240
Db	15181	TATCTCCCTCTCTTCCTCCTCTCTCTCTTAAGCCCTGATTAATTAACCTAGCTAATCTCTCT	15240
Qy	15241	ttctagtcctactgccaacctatactacaacaatagcaagccatcaccoccatccagctc	15300
Db	15241	TTCTAGTCTCTACTGCAACCTCTACTACTACCAATAGCAAGCACATCAACCCATCCAGGTC	15300
Qy	15301	atgaccctctgactgaggagctcccatcttcgaagaagcatgaaacccaagccctctatgct	15360
Db	15301	ATGACCCTCTGACTGGAGACTCCCATTTGGCTTAACGGCATGAACCCAGGCTTCCTTATAGT	15360
Qy	15361	gacacacaagaattcccaagcctcatatcatctctctgtgcacatctctgcctagaat	15420
Db	15361	GACACACAAGATTTCCAAAGCCTATCTATCTTTCTTGCCACTCTCTGCTAGCAAT	15420
Qy	15421	ctaaccttcacaaagaagaagttgagttcttccttgcaacccaagagctattctct	15480
Db	15421	CTAACCTTCACCAAGCAAGAGAGTGAAGTTCCTGTGCACCCAGAGCTATTTCTCTCT	15480
Qy	15481	ctccaatgccttgctcatatgctctccctcgaagccgaagtgcatatgctctcattgcgcc	15540
Db	15481	CTCCAAATGCCTTGGCTTATAGCTGTCTCTCAGCCAGAGAGTATGGCTTCATTTGCCCC	15540
Qy	15541	tcatttgagttcatctcaagtctcaagctcaagctgaagtgtagctctcctggaactgcatcaat	15600
Db	15541	TCATTTGAGGTTCACTCTCAAGTCTCAGCTCAAGTGTAGCTCTCTCGAAACTGTCTCATAT	15600
Qy	15601	gtcccaaggttagcacatatccctctctctctgtaacttccaaactctcatatgacaga	15660
Db	15601	GTCCTAAGGTTACATCAATACCTTTCTTCTGTGAACCTCCCAATTTCTTAATTGCAATGA	15660
Qy	15661	ctctatcgtttgcccctacataatccaacttttaatgctatcgtatagatggttgagctgctgt	15720

D	15661	CCTCATCGTTCGCCCTACACTATATTCGAACCTTTAAATGCTATCGATATGATGGTTTGCGTCGT	15722
Q	15721	gtctctaccccaactctcatcccgatctgcaccccccagtgctcaggggagagacctgtg	15780
D	15721	gtctctaccccaactctcatcccgatctgcaccccccagtgctcaggggagagacctgtg	15780
Q	15781	ggaagtgatgtatcatatgaaggcgatctccccccatgcgtctctcatgaagtgaggagt	15840
D	15781	ggaagtgatgtatcatatgaaggcgatctccccccatgcgtctctcatgaagtgaggagt	15840
Q	15841	tctcatgtgatttgaatgggtttaaagatttgacattccctctgcgtctcctctgc	15900
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D	16081	ctctctgtgaagactctctgtgaaggcgagagcgacttatgtatctaaaggcttgca	16140
Q	16141	ctgtgtgaacacatgccccacacattcatatgtttaaattctctagcctctaggccctcaag	16200
D	16141	ctgtgtgaacacatgccccacacattcatatgtttaaattctctagcctctaggccctcaag	16200
Q	16201	ttgtgacctatttgaaagagagctcggtgcagatcaattagttaatgataagatcaatgct	16260
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D	16381	tctaaagacatctcttgaaacacaaataatgccccagacacacagaaagctgacgtg	16440
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D	16621	ttaaagtattgaataatgaataaacaatgtctcttgactgtgtgaaattaccccttca	16680
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Dh	19021	AAAGCAGTCGTATAAAAATTTATTCCAAAAAATATGTATATTTGAAAGTATAGGCC	19080
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Oy	19141	tttgttataaaaagatlaagaaggcataagaatltggaatttctaactataaaggt	19200
Dh	19141	TTTTGCTAAAAAGATTAGAAGGACGATPAGATGTGATTTTACCTCATTTAAAGGT	19200
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Oy	19261	ttctgtgttaaaccaattatagctaaagaataaaggatcatccagtttctgtgaact	19320
Dh	19261	TTCTGTGTGTAAACATTAATAGCTAAAGATAAAAGTATCATCCAGTTTCTGTGAACT	19320
Oy	19321	ggacatlaaaglaaanaatgcaacaggttctctgaagcacaacctgtctttaaca	19380
Dh	19321	GGACATTTAAAGTAAAAATGCCAACAGTTTCTTGTGAAGCCACACCTGCTTTAACAA	19380
Oy	19381	aattataaaggttbaaanaagltcgtiaaanaacttaaccttaagtcbaaacatgaaat	19440
Dh	19381	AATTATTAAGGTTTAAAAAGAGTCTGTAAAACTTAACCTTAAGGTCAACATGAANAATT	19440
Oy	19441	ggataaataatgtctatgtaggttcttlaaanaatlaagtttaaacatlaatacacacta	19500
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Oy	19501	taagtgtaaaattatgacttatacttggtataaaaaatacatacaagaagtattataata	19560
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Oy	19561	aatggttttagcttctctgtgtgtccttaaaaacttaaaaataggtccctaaagaaact	19620
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Oy	19621	catlctactagaagatcatalagaagtlaaagacttlaaanaaactlttgcaattaaagacag	19680
Dh	19621	CATTTACTAGAGGATCATAGAAAGTTAAAGACTTAAACAAACTTTGGCAATTAAGACAG	19680
Oy	19681	cataccagaatgcaaatgctgtgttgaatggatcaaatatcatcactgtgcacattaaca	19740
Dh	19681	CATACCAGATGCCAATGCTGCTGTGAATGATCAAAATATTCATCTGTGCACATTAAACA	19740
Oy	19741	aaagaagtgttatctctgtgtgacgttgagagccagaagccctatgtgccccctcac	19800
Dh	19741	AAAGAGTGTATCTCTGTGTGCACATGAGAGGCCAGAGCCCTCATGTGCCCTTCCAC	19800
Oy	19801	taaagtgtcctcccaagtcaccacagacgtgtgagtgacatgtcttccagaagttcta	19860
Dh	19801	TAAATGTGCTCCACAGTCCACAGGCGTGGCGTGCATGTACTCTTTTCCAGATTTCTA	19860
Oy	19861	cagccttgagtaataagtaatgcacaaactctctgtctataccctgttgggtcagcccca	19920
Dh	19861	CAGCTTGAGTATTAAGTATAGTCACAAACTCTCTGTCTATCCCTGTGGGTGAGCCCCGA	19920
Oy	19921	gggcatccagcctccgtctcccaacaataagttcaactcatgtctctcacaagaagag	19980
Dh	19921	GGGCATCCAGCCTCCGCTCCCAACACTAAATTTCACTCATGTCTCTCCACACAGAGAG	19980
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LOCUS	HS313L4	128230 bp	DNA	PRI	23-NOV-1999							
DEFINITION	Human DNA sequence from PAC 313L4 on chromosome 1q24. Contains ESTs.											
ACCESSION	Z99943											
VERSION	Z99943.1	GI:2887308										
KEYWORDS	1q24.											
SOURCE	human.											
ORGANISM	Homo sapiens											
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.											
AUTHORS	1 (bases 1 to 128230)											
TITLE	Pearce,A.											
JOURNAL	Direct Submission											
COMMENT	Submitted (12-NOV-1997) Chromosome 1 Project Group (http://www.sanger.ac.uk/HGP/Chrl/) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk On Feb 14, 1998 this sequence request replaced gi:2578084. IMPORTANT: This sequence is the entire insert of clone 313L4. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above. This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre chromosome 1 mapping group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl/ This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The true left end of clone 313L4 is at 1 in this sequence. The true left end of clone 295C6 is at 12237. The true right end of clone 313L4 is at 128230. 313L4 is from the library RPCI1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ . Location/Qualifiers											
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	/note="20 copies of 2 mer 88 % conserved"											
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repeat_region 7732..8034
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repeat_region 29924..30226
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repeat_region 30296..30594
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repeat_region 31058..31167
/note="MER5B repeat: matches 31..134 of consensus"
repeat_region 31174..31438
/note="LIMC1 repeat: matches 1064..787 of consensus"
repeat_region 32457..32723
/note="AluY repeat: matches 294..1 of consensus"
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/note="match: 5' EST W39755 clone 328608"
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H08848; match: R64027 R39393 AA291124"
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Query Match 29.4% Score 5877.2; DB 11; Length 128230;
Best Local Similarity 99.98; Pred. No. 0;
Matches 5891; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

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QY 61 tagatccactagaggttcagggtctgtcatcatcatctcatatccaaagggagaa 120
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ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	1 (bases 1 to 7728) Schulte,A.M., Lai,S., Kurtz,A., Czudayno,F., Riegel,A.T. and Wellstein,A.	
TITLE	Human trophectoderm and chorioncarcinoma expression of the growth factor pleiotrophin attributable to germ-line insertion of an endogenous retrovirus	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 93 (25), 14759-14764 (1996)	
MEDLINE	97121462	
REFERENCE	2 (bases 1 to 7728) Schulte,A.M. and Wellstein,A.	
AUTHORS	Structure and phylogenetic analysis of an endogenous retrovirus inserted into the human growth factor gene pleiotrophin	
JOURNAL	J. Virol. 72 (7), 6065-6072 (1998)	
MEDLINE	98285768	
REFERENCE	3 (bases 1 to 7728) Schulte,A.M. and Wellstein,A.	
AUTHORS	Direct Submission	
TITLE	Submitted (10-APR-1998) Pharmacology, Georgetown University Medical Center, 3970 Reservoir Road, Washington, D.C. 20007, USA	
JOURNAL	On Oct 27, 1998 this sequence version replaced gi:1778411.	
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 SOURCE human.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 135305)
 AUTHORS Patel, R.
 TITLE Direct Submission
 JOURNAL Submitted (09-SEP-1999) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonequery@sanger.ac.uk
 On Sep 6, 1999 this sequence version replaced gi:5791529.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found they are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMBASE; Information
 on the WORMBASE database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence is
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COMMENT


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QY 19610 aaggaacaactcatttactcagagatcataagaagttaaagaacttaacaacttggc 19669
Db 31427 AAGAAAAACATTCATTTTCTAGAGGATCAATAAAGTTAAAGACTT-----AACTTTAGC 31373
QY 19670 aatcaagacagcaccacaagaatcaaatgacctgttgtaaatgatacaatctccatctg 19729
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Db 31312 CACGTTAAACAAAGCAATGTTATGCTTGTGCACATGAGCAGCCAGGCCCTGATGTG 31253
QY 19790 cccctctccactaaatggtgtccctccagtcacccaagcgtgtgtgcatggttactctt 19849
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QY 19850 ccaggaattcacaagcctgagagtaataagtcataccaaactctctctcctc----- 19900
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QY 19900 tccctgtgggtcagcccccagagggccatccagctcgtctcccaactaagttcaatt 19959
Db 31132 TCCCTCGGGGTACGCTCCGAGGGCCATCCAGCTTCGCTCTCCCAACTAAGTTCACTT 31073
QY 19960 catgtctctccacacagagaagaacttaggtatccttgya 20000
Db 31072 CGGTCTCTCACGCGTGGGAGGAGACTTAGCATTCCTTGA 31032

RESULT 5
AC011036
LOCUS Homo sapiens clone 7_E_18, *** SEQUENCING IN PROGRESS ***, 7
DEFINITION
AC011036 137413 bp DNA
VERSION AC011036.2 GI:6139104
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 137413)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone 7_E_18
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 137413)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Balwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhaltier,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collamore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domino,M., Donnell,L., Doyle,M.,
Ferreira,P., Fitzhugh,M., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howard,J.C., Johnson,R., Jones,C., Kamp,L., Karas,A., Klein,J.,
Lehoczky,J., Lileu,C., Locke,K., MacDonald,P., Margulis,N.,
McEwan,P., McQuirk,A., McKernan,K., McLaughlin,V., Melair,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
JOURNAL Direct Submission
COMMENT Submitted (30-SEP-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Oct 29, 1999 this sequence version replaced g1:6002002.
All repeats were identified using RepeatMasker: Smit, A.F.A. &
Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 2686: contig of 2686 bp in length
* 2687 gap of unknown length
* 10073: contig of 7387 bp in length
* 10074 gap of unknown length
* 18819: contig of 8746 bp in length
* 18820 gap of unknown length
* 31867 gap of 13047 bp in length
* 56808: contig of 24942 bp in length
* 56809 gap of unknown length
* 90490: contig of 33682 bp in length
* 137413: gap of unknown length
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* Location/Qualifiers
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/db_xref="taxon:9606"
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FEATURES

source


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QY 19454 tatgaggtttatataaattagtttaacattataaacaacataataaaggttaaat 19513
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QY 19977 agaggaacttagagattccttga 20000
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Db 59967 GGAGAAACTATGATCTCTGGA 59990

RESULT 6
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LOCUS Homo sapiens clone NH0218P06, *** SEQUENCING IN PROGRESS ***, 2
DEFINITION unordered pieces.
ACCESSION AC010877.2 GI:6175241
VERSION AC010877.2
KEYWORDS HTG; HTGS-PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 138088)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 138088)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (25-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Nov 2, 1999 this sequence version replaced gi:5923733.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 66357: contig of 66357 bp in length
* 66358 66375: gap of unknown length
* 66376 138088: contig of 71713 bp in length.
FEATURES
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/db_xref="taxon:9606"
/clone="NH0218P06"
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Best Local Similarity 77.6%; Pred. No. 3,7e-291;
Matches 2310; Conservative 0; Mismatches 467; Indels 198; Gaps 22;

QY 17060 agagacagaccctcatatgttttatactcaag-----aaaaggaagaagaagt 17109
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Dh 17011 AATTAAGCC-CTTCTTTTACAACTCGGTATCTGAGAGCTTTTACAGCGGTCTCTG 17069
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Qy 17590 cttagcgagcttagcctgcccctgtgaaacatccctgctgggagctccaacagccag 17649
Dh 17130 CTTAG-----GCCGCGCTGGGAGCATCCCTCGAGGGGACTCCGGCCAGCTGAG 17180
Qy 17650 tgaagcgatcctgagagctctcctggttaggcatggcccggtggagacacctcgccag 17709
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Qy 17710 agcagtggtgagcagcccggtgagagatcaacagagtggtcgtgaaacccggaaagat 17769
Dh 17240 AGCAGCGGTAGCAGGCGCCCTGCAAGAGATCAGCAGATGGGTGAACACAGGAAGAAC 17299
Qy 17770 tggcacttgagctcggagaaactaaacttgtaagactgcttggaactgccc-cac 17828
Dh 17300 TGGACCTTGGAGTGGACATCTGAACTTGTAAGTACGTCTTGGAACTTGGCACAC 17359
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Dh 17700 AGCTTAGT 17759
Qy 18248 aactatgttgaaaaa--tttcaagaaagagatlaagggagaattacggtgttactatga 18305
Dh 17760 AACTATGTTAAATAATTTTCAAGAAAGATTTAAAGAGATTAAGGAGTACTACTGTACA 17819
Qy 18306 ctgaaaaaacttaagacttgtgtaaaatagactggcccaaatatagaggtgtgtgtgtgca 18365
Dh 17820 CTAGGAAAACTTAGACTTGTGTGAATAGACTGGCCAGAGTTAGAGGTGGGTGGCCA 17879
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Qy 18482 ctgccccccagtagttaaagagagcagaagaagagaaagaaacagagcaaaagaa 18541
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Qy 18542 agtcagaagagagagagagagagagagacaagaatgcaaaagtagaagaaagaaatag 18601
Dh 18031 CAGCAGCATTAAGCGGCTGGCAGAGCAAGAAACCAACGACAGAGAAACGA----- 18084
Qy 18602 agagaataataccagtagttaagaaaaaatagtgtaacctatccctttaaagccag 18661
Dh 18084 --GGCCATCTATCAATTAATTAAGTTTGAATTAAGTAAACAGGCTTAGCAAAAGTAT 18141
Qy 18662 gtaatttaaaacctaataattgataattaaaggtatctccgttaacctgttaacctta 18721
Dh 18142 TAAATCTCAAACTTACA-----GTTTTCAGTAAAGTGAAGTTTGCTA 18187
Qy 18722 ataccacttggtttagtgaacaagcgatcccgaaagcactgagccctccat 18781
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Qy 18782 caaaaatccctaaccagtaaccacagagatggccagatgcatccaatcgttagcagcag 18841
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Qy 18842 ctgcttctaacaggaataaaaaaaagagctgtggtggaagcaaaattatgttaa 18901
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Qy 18902 aagatgtatattgtaaatcttctgtgaataaataatcttgtttaaagaagaa 18961
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Qy 19136 tatacttggtaaaagatlagagagagcagataagaatgtgtaatttactcatataa 19195
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Qy 19196 aaggttaaaaaaatattgttttgaagtttaagcaagttttaaagtgtaattgtlaaa 19255
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Dh 18666 AAAAATCTGTGTATACCAATATAGCTAAAGTTAAAAAATATATCATCCAGTTCTGCT 18725
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Dh 18726 GAACCTACATTAAGTAAAGTAAATGCAACAGCTTCTTTAAGCATCAACCTGCTCTTTA 18785
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Db	89063	ATTCATCTGCACGTTAAACAAGCAATTGTATGCTTGACACATGGCAGCGCAGGG	89122
OY	19780	cacctatgtcccccttcacataagtgtctctccacgccagggcgttgccgatgg	19839
Db	89123	CCCTGATGTGTCTCCCTTACTAATAGGTGTCCTCCAGTCGACGACGATGGGCTGCATGG	89182
OY	19840	tactctttccaggatctcacagccttggagtaataagtcacgtccaactctctcta	19899
Db	89183	TAGCTCTTTCCAGATCTCATAGCCTGAGTAGTAAGTCATGCCAACGCTCTCTGCTA	89242
OY	19900	-----ccctctgyggctcaagccccggagggccatccagcctcogtcccacaact	19949
Db	89243	TATCCTGAAGTCCCTGCAGGCTACGCCCCGAGGGCTATCCAGCTTCTCTCTAACACT	89302
OY	19950	aagttcaactatgtctctccacacagagaagaaacttagatctccttga	20000
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LOCUS	AC008554	227567 bp DNA HTG	31-OCT-1999
DEFINITION	Homo sapiens chromosome 19 clone C1F-HSPC_513N18, *** SEQUENCING IN		
ACCESSION	PROGRAMS ***	100 unordered pieces.	
VERSION	AC008554		
KEYWORDS	AC008554.2 GI:6165166		
SOURCE	HTG; HTGS_PHASEI.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
JOURNAL	Eutheria; Primates; Catarrhini; Homidae; Homo.		
REFERENCE	1 (bases 1 to 227567)		
AUTHORS	DOE Joint Genome Institute.		
JOURNAL	Sequencing of Human Chromosome 19		
AUTHORS	Unpublished		
JOURNAL	2 (bases 1 to 227567)		
AUTHORS	DOE Joint Genome Institute.		
JOURNAL	Direct Submission		
AUTHORS	Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint		
JOURNAL	Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA		
COMMENT	On Oct 31, 1999 this sequence version replaced gi:5686513. www.jgi.doe.gov. NOTE: This is a 'working draft' sequence. It currently consists of 100 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.		
*	1	318: contig of 318 bp in length	
*	319	gap of unknown length	
*	885	contig of 568 bp in length	
*	887	gap of unknown length	
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*	1783	gap of unknown length	
*	2247	contig of 465 bp in length	
*	2248	gap of unknown length	
*	2470	contig of 223 bp in length	
*	2471	gap of unknown length	
*	2638	contig of 168 bp in length	
*	2639	gap of unknown length	
*	3193	contig of 555 bp in length	
*	3194	gap of unknown length	
*	3925	contig of 733 bp in length	
*	3927	gap of unknown length	
*	4631	contig of 705 bp in length	
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*	5675	contig of 1044 bp in length	
*		gap of unknown length	
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*	7039	7992: gap of unknown length	
*	7993	8501: gap of unknown length	
*	8502	9192: gap of unknown length	
*	9193	9921: gap of unknown length	
*	9922	10917: gap of unknown length	
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*	16504	16857: gap of unknown length	
*	16858	17470: gap of unknown length	
*	17471	18225: contig of 755 bp in length	
*	18226	18896: gap of unknown length	
*	18897	20001: gap of unknown length	
*	20002	20423: gap of unknown length	
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*	21075	21636: contig of 562 bp in length	
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*	22742	23249: contig of 508 bp in length	
*	23250	23909: gap of unknown length	
*	23910	24765: contig of 856 bp in length	
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*	25962	26615: gap of unknown length	
*	26616	27017: gap of unknown length	
*	27018	27743: contig of 726 bp in length	
*	27744	28040: gap of unknown length	
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Db	200302	CCACAGTGTGCCTGCATTTGGACACTTTTG-TTCTGTTTTGACCTGACCTTGAAGTCACTGA	200244
OY	18050	tacttggtttctgtgttttggacctgtgtgattcttgaatactcttgatttggtttgat	18109
Db	200243	TACTTAATTTTTGGTTTTGGACCTGGCTTAGATTTCTGGATACCTGTGATTTTTGGTTTTGAT	200184
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OY	18161	-ttgtttctgtgtgtgtgcacgtgtgtgtgtgagagtgtgttttcttcgagaagaacatggt	18219
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OY	18519	ggaagaacagagccaaagaagaagtcaagaagagagagagggagagagagagacagaa	18578
Db	199777	-----GAAACAGACGCTTAAGCCGCTGGCAGAGGCAAGAAACACC	199738
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Db	199679	-----TCTTATTTAATACCAAGGGTAAATGAATCCCAAA-----	199644
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JOURNAL	Fu, Y., Pan, H., Mcdermid, H. and Roe, B. A.	
REFERENCE	Homo sapiens BAC Clone b128f11	
AUTHORS	Unpublished	
TITLE	2 (bases 1 to 226345)	
JOURNAL	Fu, Y., Pan, H., Mcdermid, H. and Roe, B. A.	
REFERENCE	Direct Submission	
AUTHORS	Submitted (08-AUG-1998) Department of Chemistry And Biochemistry,	
TITLE	The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,	
JOURNAL	OK 73019, USA	
REFERENCE	3 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermid, H. and Roe, B. A.	
TITLE	Direct Submission	
JOURNAL	Submitted (10-SEP-1998) Department of Chemistry And Biochemistry,	
	The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,	
	OK 73019, USA	
REFERENCE	4 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermid, H. and Roe, B. A.	
TITLE	Direct Submission	
JOURNAL	Submitted (23-SEP-1998) Department of Chemistry And Biochemistry,	
	The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,	
	OK 73019, USA	
REFERENCE	5 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermid, H. and Roe, B. A.	
TITLE	Direct Submission	
JOURNAL	Submitted (01-OCT-1998) Department of Chemistry And Biochemistry,	
	The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,	
	OK 73019, USA	
REFERENCE	6 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermid, H. and Roe, B. A.	
TITLE	Direct Submission	
JOURNAL	Submitted (04-OCT-1998) Department of Chemistry And Biochemistry,	
	The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,	
	OK 73019, USA	
REFERENCE	7 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermid, H. and Roe, B. A.	
TITLE	Direct Submission	
JOURNAL	Submitted (14-OCT-1998) Department of Chemistry And Biochemistry,	
	The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,	
	OK 73019, USA	
REFERENCE	8 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermid, H. and Roe, B. A.	
TITLE	Direct Submission	
JOURNAL	Submitted (05-NOV-1998) Department of Chemistry And Biochemistry,	
	The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,	
	OK 73019, USA	
REFERENCE	9 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermid, H. and Roe, B. A.	
TITLE	Direct Submission	
JOURNAL	Submitted (11-NOV-1998) Department of Chemistry And Biochemistry,	
	The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,	
	OK 73019, USA	
REFERENCE	10 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermid, H. and Roe, B. A.	
TITLE	Direct Submission	
JOURNAL	Submitted (21-NOV-1998) Department of Chemistry And Biochemistry,	
	The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,	
	OK 73019, USA	
REFERENCE	11 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermid, H. and Roe, B. A.	
TITLE	Direct Submission	
JOURNAL	Submitted (26-NOV-1998) Department of Chemistry And Biochemistry,	
	The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,	
	OK 73019, USA	
REFERENCE	12 (bases 1 to 226345)	
AUTHORS	Fu, Y., Pan, H., Mcdermid, H. and Roe, B. A.	

TITLE	Direct Submission
JOURNAL	Submitted (19-JAN-1999) Department of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
REFERENCE	13 (bases 1 to 226345)
AUTHORS	Fu,Y., Pan,H., McDermaid,H. and Roe,B.A.
TITLE	Direct Submission
JOURNAL	Submitted (24-JAN-1999) Department of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
REFERENCE	14 (bases 1 to 226345)
AUTHORS	Fu,Y., Pan,H., McDermaid,H. and Roe,B.A.
TITLE	Direct Submission
JOURNAL	Submitted (09-APR-1999) Department of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
REFERENCE	15 (bases 1 to 226345)
AUTHORS	Fu,Y., Pan,H., McDermaid,H. and Roe,B.A.
TITLE	Direct Submission
JOURNAL	Submitted (22-APR-1999) Department of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
REFERENCE	16 (bases 1 to 226345)
AUTHORS	Fu,Y., Pan,H., McDermaid,H. and Roe,B.A.
TITLE	Direct Submission
JOURNAL	Submitted (24-APR-1999) Department of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
REFERENCE	17 (bases 1 to 226345)
AUTHORS	Fu,Y., Pan,H., McDermaid,H. and Roe,B.A.
TITLE	Direct Submission
JOURNAL	Submitted (12-OCT-1999) Department of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
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Db	224977	TAAAAAGGCTTAATAAAATCTTAC--ATGTCATAACATTAATAAAATTGGATTAATATGTC	225033
QY	19454	catgaggtcttatcaaaatgaagttacaattaaatacacctcaataataaaggtaaagt	19513
Db	225034	TACAAAGGTTTTATTATAAATTAAAGTTAAACATTA-----ACACTATATTAAAGGTAATAAT	225088
QY	19514	tagcttatctgtgtaaaaaatcatalacaagaagtatttaatatataaaatgtygtttagc	19573
Db	225089	TAACTATTGTGTGTAAAAAATCATACAAAGAGCTTTTATTAATATATAAATGAGTTTAGC	225148

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QY 19574 tttcttggtctaaactaaataaagagtcctaaagaaacttattttactagag 19633
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QY 19634 gatcataagaagctaaagactaaacaacttggcaattaaagacacataccaagatgc 19693
Db 225209 GATCATAGAACTAAAGACTTAAACAAACTTGGCAATTAAGACAGATCAACCAAGATGC 225268
QY 19694 aaatgcttggttgaagaatgatcaaatatcattcattgcacattaaacaaagcagtgtta 19753
Db 225269 AAAGCCGCTGTAAGTAATGAGTAATATTCATCTGCACGTTAAACAAAGCAATGTGTA 225328
QY 19754 tgccttgacacatggcagagcagagccctatgttccccccttcacataaagtgtcttc 19813
Db 225329 TGCTTGTGCAATAGGACAGAGCCCTGATTTTCCCTCCACTAAGGTGCTTC 225388
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QY 19924 ccacccagccctcgctctcccaactaaagtctcattcattcctcaccacagagagagaa 19983
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Db 225569 ACTTAGATCTCTTGA 225585

RESULT 10
AC004185 36921 bp DNA PRI 24-NOV-1998
LOCUS Homo sapiens clone UMGc:y14c094 from 6p21, complete sequence.
DEFINITION AC004185
VERSION AC004185.1 GI:3924650
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 36921)
AUTHORS Guillaudoux,T., Janer,M., Wong,G.K., Spies,T. and Geraghty,D.E.
TITLE The complete genomic sequence of 424,015 bp at the centromeric end
of the H1A class I region: gene content and polymorphism
Proc. Natl. Acad. Sci. U.S.A. 95 (16), 9494-9499 (1998)
JOURNAL 98356185
MEDLINE Fred Hutchinson Cancer Research Center
REMARK The Clinical Research Division
1100 Fairview Ave. N., P.O. Box 19024
Seattle, WA 98109-1024
2 (bases 1 to 36921)
REFERENCE Geraghty,D.E. and Olson,M.V.
AUTHORS Direct Submission
TITLE Submitted (23-FEB-1998) Human Genome Center, University of
JOURNAL Washington, Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 36921)
REFERENCE Geraghty,D.E. and Olson,M.V.
AUTHORS Direct Submission
TITLE Submitted (24-NOV-1998) Human Genome Center, University of
JOURNAL Washington, Box 352145, Seattle, WA 98195, USA
COMMENT On Nov 24, 1998 this sequence version replaced gi:2905875.
overlapping sequences:
5': UMGc:y3c062
3': UMGc:y14c057
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Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.

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Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the Genbank flat file format but are available as part of this entry's ASN.1 file.

Double stranded (DS) coverage: 92.5%
DS or two chemistry coverage: 100.0%
Single stranded regions: 0

Sequence Validation:
This sequence has been validated by Multiple Complete Digest Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below.
Small fragments below a variable cutoff (approximately 400-600bp) are not mapped and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by dashed lines.

Map	Seq	HindIII		NsiI	
		Map	Seq	Map	Seq
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5171.90	5169.00	11619.04	11518.00	17878.57	17883.00
1127.00	1117.00	12730.55	12691.00	2714.05	2641.00
4366.19	4286.00				
8749.71	8563.00				
927.50	911.00				
2295.76	2284.00				

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/cell_line="CGM1"
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/rpt_family="Alu"
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2898..3138
/rpt_family="L1"
3682..3965
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4029..4531
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4767..4847
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complement(5298..5406)
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complement(5993..6291)
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6061..6302
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Best Local Similarity	74.8%	Pred. No. 1.4e-259;						
Matches 2249;	Conservative	0;	Mismatches 424;	Indels 332;	Gaps 22;			
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DB	32870	TTCCCTTTGAGGAGAGAGACCCTTCGATGTATTATGCTTTATCTACATA	32929					
QY	17097	-----aggaagaagaagyaataaaggcaatgagcccgcgcttaggaaccaagccg	17151					
DB	32930	TCTGTTTAAAGAAAACAAAGGAAGTAAACCAAGACAGCAGCCTCGCCGACAGCCA	32989					
QY	17152	aaacaaagcccttggccctgacccaacaaagctcgtagttaaatcgacccctgacctg	17211					
DB	32990	AAACCAAGCGCTGGCGCTCGCTTAACCAACGAGTAGTAAAAATCAACCATGACTTAG	33049					
QY	17212	caacgttgttactcatgatatccagaaatgtaatggaagggcatltgatatgaagaaat	17271					
DB	33050	AACGGAGTAGTATTCCTAGTTTCAGCA-----CATGTATGAAGAAACAT	33094					
QY	17272	tgtgaatctcctcgtctcgtctgttcttctacagtgaaccaagtgctccaaagccctgtca	17331					
DB	33095	TGTGACAGTCCCTGCCCTGTTCTGTCTGTCTGTACACACAGTGATGCACCCCTGTCA	33154					
QY	17332	cgtaaccccttgctactcaatcgatcgacaagccctctcatgycgaagcccccctgaagtgt	17391					
DB	33155	CGTACACACTGGCTACTCAATTCATTCACGACACTTTCATG-TGAATCTTAGGTGT	33213					
QY	17392	ggagcccttaaaaggagaaggttagagtaagacagagctcgattttagaagcttagcc	17451					
DB	33214	GAGACCTTAAAGGAGACAGAAATTTGTGCAATTCAGGAGATTGGATTTAAGCAGTACT	33273					
QY	17452	tgcgcatctcccaagctgattaaagccacccctcactcatctcgtgtcctgagggttt	17511					
DB	33274	TGCCGATGCTCGACACTGAATAAAGCC-CTTCCTTCTACAACTCGGTGTGAAAGGTTT	33332					
QY	17512	tgtctggggctcatctcgtctacatttcttgtttccctgaacgggaagcaagtattaac	17571					
DB	33333	TGTCGGGGCTCGTCTCTCAATTTCTTGGTTCCTGTAAGAGAGGAGGTAACGTAC	33392					
QY	17572	agatgctgaggaagcaagctccttaagcgggtcttaagccctgcgttgaacatcccgctgg	17631					
DB	33393	GAGCGGCCAAGGACACCCCTTGGGTGAGCCTTAGCCCTGCTGAGAGATCCCTGCGGTG	33452					
QY	17632	gactcaaaccaagcaagtagacggagatcctctagaagctctccctggtatgacattgcccc	17691					
DB	33453	GACTGTGGCCAGCCGATGATGACGC-GATCCAAAGAGCGCTCCCGGTGGAATAATCCCG	33511					
QY	17692	ggttggaaacctcgccaaagagtggttgggaagggcccccgagggaatcaacaagaagggc	17751					
DB	33512	GGTGAAAGCCTTCGCAAGAGACGACGTAAGAGGCCCCCGAGGAGATTAAACAACGTGC	33571					
QY	17752	tgaacaacgggaagaaatcttgcacttgtgagtcggaacacaaacttgytgaagctagt	17811					
DB	33572	TGAACACTGGGAAGAACTGGACATTGGAAGTCCGAGACTCGAACAACCTTGTAACATAAGT	33631					
QY	17812	ctttggaacttg-cccactcatlttagtggaaagatgacctgatacccaagcgctgccc	17870					
DB	33632	CTTTGGAACCTTGCCCACTCATCTGATGTGAAGACATGGCTGTGATCACCCCATGTGTTGCC	33691					
QY	17871	tttatacgaacttgatttcttggttttgaacttggttgaattacttgaaagsgactgctctg	17930					
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QY	19346	gtttctcttgaagcaccacacgcgtcctttaacaaaaattataaagggttaaaagagct	19405
Db	34928	GTTTTCCTTAAGCATCAACGCGCTTTAACAAAAATTATTAAGGTATAAAGAGCT	34987
QY	19406	gtaaaaacttacctatgtgtcaacaatgaaaaattggaataatgtctatgaagttta	19465
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QY	19466	ttaaaattgaagtttaccatttaataaacacacaaatataaagtgaaatttagcttaccg	19525
Db	35048	TTAAAAATTATGTTTACATTTAATAACACATTAATTAAGGTAATAATTTAGCTTACCTGG	35107
QY	19526	tataaaatcatcacagaagttataataataaactggtgttacccttctgtgtct	19585
Db	35108	TTATAAATCATACAGAAGCATTTTATAATATAAAGGTGTAGCTTTCTTGGTCT	35167
QY	19586	aaaaactaataaaataggtccctaaaggaacatcttacttaagagatcatagaagt	19645
Db	35168	AAAACTAATAAATAGATGCTAAGAGAAACATTCATTACAGAGATCATAGAGT	35227
QY	19646	taaaagactaaacaactttggtcaataagaacgcatacaagaatgtcaaatgctgtt	19705
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Db	35288	GGAATGGATTAAATTTCTCATCTGTGACGTTAAACAAATCATTTGTTATGCTGTGACA	35347
QY	19766	tggcagccagagggccctcatctgtcccccctccactaaagtgtctccagtcacacagg	19825
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QY	19886	aactctctctgtcta-----tccctgtgggttcagccccccagggccatccagcctc	19935
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QY	19936	cgtctcccaacaactaagttcaacttcatctctcaccacagaggaacttaagattcc	19995
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VERSION AC006047.1 GI:3924651
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 37139)
AUTHORS Guillaudeau,T., Janer,M., Wong,G.K., Spies,T. and Geraghty,D.E.
TITLE The complete genomic sequence of 424,015 bp at the centromeric end
of the HLA class I region: gene content and polymorphism
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (16), 9494-9499 (1998)
MEDLINE 98356185
REMARK Fred Hutchinson Cancer Research Center
The Clinical Research Division
1100 Fairview Ave. N., P.O. Box 19024
Seattle, WA 98109-1024
2 (bases 1 to 37139)
Geraghty,D.E. and Olson,M.V.
REFERENCE Direct Submission
AUTHORS Submitted (24-NOV-1998) Human Genome Center, University of
TITLE Washington, Box 352145, Seattle, WA 98195, USA
JOURNAL Overlapping Sequences:
COMMENT 5': UMGC:Y14C094 (Genbank Accession: AC004185)
3': UMGC:Y24C027

Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
Genbank flat file format but are available as part
of this entry's ASN.1 file.

Double stranded (DS) coverage: 79.7%
DS or two chemistry coverage: 99.9%
Single stranded regions: 2

Sequence Validation:
This sequence has been validated by Multiple Complete Digest
Mapping. Comparison of the experimentally derived map digest
fragments with sequence-predicted fragments is given below.
Small fragments below a variable cutoff (approximately 400-600bp)
are not mapped and hence do not appear in the table. There are no
significant remaining discrepancies between the experimental and
predicted values. Uniquely ordered fragment groups are separated
by dashed lines.

Map	Seq	Map	Seq	Map	Seq
BglII		HindIII		NsiI	
927.50	911.00	3626.98	3542.00	2714.05	2641.00
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		979.90	957.00	2968.55	2927.00
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VERSION AP000509.1 GI:5926696
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REFERENCE
AUTHORS Shina,S., Tamiya,G., Oka,A. and Inoko,H.
TITLE Homo sapiens 2,229,818bp genomic DNA of 6p21.3 HLA class I region
JOURNAL Published only in Database (1999) In press
REFERENCE
AUTHORS Hirakawa,M., Yamaguchi,H., Imai,K. and Shimada,J.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1999) to the DDBJ/EMBL/GenBank databases. MIKA
Hirakawa, Japan Science and Technology Corporation (JST), Advanced
Databases Department, 5-3, Yonbancho, Chiyoda-ku, Tokyo 102-0081,
Japan (E-mail:mika@tokyo.jst.go.jp,
URL:http://www-alis.tokyo.jst.go.jp/, Tel:81-3-5214-8491,
Fax:81-3-5214-8470)
COMMENT This sequence is conducted by Tokai University as a JST sequencing
Team.
Principal Investigator: Hidecoshi Inoko Ph.D
Phone:+81-463-93-1121. Fax:+81-463-94-8884,
The sequence is submitted by Human Genome Sequencing in ALIS
project of JST
Japan Science and Technology Corporation (JST)
5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0081 Japan
For further information about this sequences, please visit our
sequence archive Web site (http://www-alis.tokyo.jst.go.jp/HGS/top.
html) or send email to webmaster@www-alis.tokyo.jst.go.jp.

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TITLE Nucleotide sequence analysis of the HLA class I region spanning the
JOURNAL 237 kb segment around the HLA-B and -C genes
REFERENCE Unpublished (1996)
AUTHORS 3 (bases 1 to 236822)
TITLE Inoko, H.
JOURNAL Direct Submission
Submitted (10-APR-1996) to the DDBJ/EMBL/GenBank databases.
Hideooshi Inoko, Tokai University School of Medicine, Molecular
Life Science; Bohseidai, Isehara, Kanagawa 259-11, Japan
(E-mail: hinoke@is.jcc.u-tokai.ac.jp, Tel: 0463-93-1121,
Fax: 0463-94-8884)
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
AUTHORS	Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	Slms.S.		
JOURNAL	Submitted (10-SEP-1999) Wellcome Trust Genome Campus, Hinxton,		
COMMENT	CambridgeShare, CB10 1SA, UK. E-mail enquiries: humquest@anger.ac.uk		
	On Sep 12, 1999 this sequence version replaced g1:5777438.		

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known: 800 n's separate segments. Unfinished: djl114E20 Contig_ID: 00340 acc-AL109912 Length: 64335 bp Unfinished: djl114E20 Contig_ID: 00618 acc-AL109912 Length: 18869 bp Unfinished: djl14E20 Contig_ID: 00619 acc-AL109912 Length: 13302 bp.

* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will be preserved.

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BASE COUNT	
ORIGIN	

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QY	17393	agcccttaaaaggacagaagtgtgacactcaagaagctcggaatttgaagcctagcct	17452
Db	67156	GCCCCCTTAAAGAGATGAATATTGTGCACCTCAGAGACCTCGGATTTTAAGCATAGTACCT	67097
QY	17453	gccgaattctccagaatgtatgaagcactcccttcaatactcvgtgtctgaagggtttt	17512
Db	67096	GCCGATGCTCCAGCTGATATAAGCC--CTCCCTTCAAACTTGCTGTGCTGAGAGTTT	67038
QY	17513	gtctgagcgtatctctgttaacttcttctgttcccttgacccgggaagcagaagtataa	17572
Db	67037	GTCTCAGCTCTCTCTGTACTATTTTGTGTCCTGTACTGGGAAACGAGGTACTGATG	66978
QY	17573	gatgttcagagcagctctcttagccgctttagccctgtfgaacaacctgtctggg	17632
Db	66977	GATGGCTGAGGAGCCCTTAGGGGCTTAAGCCTTGCCCTGTGAGCATCCCTCGGGGG	66918
QY	17633	actccaacacgcagagatgtgacgtcggaatccctgagactctccgtgttagcatttgcgcg	17682
Db	66917	ACTCCGGCCAGCCTTAGTGCCGC--GATCCAAAGAGGCTCCCGGGTAGGAAATTTCCCA	66859
QY	17693	gtggaacacctgcgcagagcaagtgtgtgacagcccccggtgagatcaacagagtgtct	17752
Db	66858	GTGGAACGCTACACAGAGCACCCGCTAGACGCCCCCATGAGGATTAACACAGTGGCT	66799
QY	17753	gaacacccgggaagaaatttggcaatttggagctccggacaactaaacttggtaagctagtct	17812
Db	66798	GAAACCCAGGAAGAACTGTGGCTTTTGGAGTCTGATATCTGAAACTTGTAAGACTAGTC	66739
QY	17813	tttgaaccttg--ccacatcccatttagatggagaagactgtgcctatcacccagcgctgct	17871
Db	66738	TTTGGAACTGTGCCCACTCCATCTCATGTAGTGAAGCGCTGGCTGTATCACCAACGCTGTGCT	66679
QY	17872	ttatcaaca--cttggtttgtgttgaacttgaacttgaacttgaacttgaagagctgtctg	17930
Db	66678	GTATTGGCAACCTTTTCTGTGTGTGTGACTTGGCTTG---ACTTGTGTGACTACTCTTT	66623
QY	17931	ggaacttgcacatccattccacatcttagttagtgaagacatgtgcatactgttcac	17990
Db	66622	GGAACCTTAC-----CCCACTCCACTGATGTGGAAGCGTGGC-----CTGATCAC	66578
QY	17991	caaggtgtgtccgtgtccgcgcaacttgtgttcttgttttgaacttgaacttgaacttgcgat	18050
Db	66577	CACGGTGTGCGCTGATGTGGACACTTGTGTCTAG--TTTGACTTGACTGTAATGTCTGAT	66519
QY	18051	acttgtgttgggttttgaacctgtgcgttggatcttcgaatacctctgatttggttgat	18110
Db	66518	ACTTTTGTTTGGTTTGTATGACCTGGCTGTGGATTTCGGAACCTCTAATTTTGGTTTGATT	66459
QY	18111	ttgtgttagtgaactcaaaagtgtgctgctcccttttaaccggtctcttctgttctg	18170
Db	66458	TTTGTTTGTGTGAACCTGCAAAAGTGTGTGTGTGCCCTTTTAACCTGTTCTTTGTTTGT	66399
QY	18171	ggtgtgcattgtgtgtgagatgtgttctgtctcgaagaacatggtgtcaggtcaaat	18230
Db	66398	GGTGTGTGTGTGTGTGACCGCTGTGTTTCTCAAAAGAACTATGCGCCAGCAACAAAT	66339
QY	18231	aagcccaacctactgaactatgttgaanaaatctcaagaagaaggtttaaggagaattac	18290
Db	66338	AAGCCCAACCCCTATGGAACCTATGTTGAAAAATTTTCAGAAAGAAATTTTAAGGACATAT	66279


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F12081 AA046699; match: F02925 AA131540 W06534 R36066
AA13383; match: AA163561 F02925 AA131540 W06534 R36066;
match: AA13383 AA163561 N89173 AA174814 AA057059; match:
AA329084 W47082 AA043955 AA341783 AA353681; match:
AA046487 AA369741 H08313 AA186895 H32730; match: H08333
H08236 N42052 D61944 R27102 N32553; match: N30431 AA307150
AA192"
repeat_region 3703..3746
/note="22 copies of 2 mer 89 & conserved"
repeat_region 4051..4183
/note="Alusq repeat: matches 1..133 of consensus;
incomplete repeat"
repeat_region 4200..4502
/note="Alusq repeat: matches 2..301 of consensus"
4659..4851
/note="Alusx repeat: matches 2..194 of consensus;
incomplete repeat"
5216..5345
/note="Aluo repeat: matches 132..1 of consensus;
incomplete repeat"
7759..7907
/note="MIR repeat: matches 174..1 of consensus"
9332..9328
/note="TIGGER1 repeat: matches 1..1472 of consensus"
9639..10335
/note="Alusq repeat: matches 1..289 of consensus"
10343..10642
/note="TIGGER1 repeat: matches 1469..2174 of consensus"
10643..10856
/note="Alusq repeat: matches 1..300 of consensus"
<10903..>16855
/note="TIGGER1 repeat: matches 2175..2417 of consensus"
10949..11384
/note="endogenous retroviral sequence"
repeat_region /note="LTR2 repeat: matches 31..449 of consensus"
15835..15870
/note="18 copies of 2 mer 83 & conserved"
repeat_region /note="18 copies of 2 mer 83 & conserved"
16856..17286
/note="LTR2 repeat: matches 31..449 of consensus"
17287..17574
/note="Alusq repeat: matches 15..300 of consensus"
18294..18650
/note="THE1B repeat: matches 358..1 of consensus"
18877..19180
/note="Aluy repeat: matches 301..2 of consensus"
19767..20013
/note="LTR2-internal repeat: matches 5002..4750 of
consensus"
repeat_region 20051..20118
/note="MIR1F repeat: matches 539..471 of consensus"
20130..20261
/note="Aluub repeat: matches 131..1 of consensus;
incomplete repeat"
20264..20722
/note="MIR1F repeat: matches 482..1 of consensus"
20858..21223
/note="MSTP repeat: matches 394..1 of consensus"
21216..21302
/note="LTR2-internal repeat: matches 4520..4433 of
consensus"
21403..21703
/note="LTR2-internal repeat: matches 3887..3580 of
consensus"
21978..22357
/note="MIR2-internal repeat: matches 3218..2839 of
consensus"
22363..22524
repeat_region /note="LTR2-internal repeat: matches 2495..2317 of
consensus"
22531..22839
/note="Alusx repeat: matches 302..1 of consensus"
23007..23309
/note="Alusq repeat: matches 3..301 of consensus"
23286..>23680
/note="STS G07544"
24008..24290
/note="STS G07436"
24008..24290
/note="Aluo repeat: matches 298..6 of consensus"
25895..26364
/note="LTR2 repeat: matches 2..449 of consensus"
26397..26697
/note="Alusq repeat: matches 1..302 of consensus"
26719..27021
/note="Alusq repeat: matches 1..302 of consensus"
29037..29334
/note="Alusx repeat: matches 300..3 of consensus"
30028..30310
/note="Alusx repeat: matches 1..301 of consensus"
30402..30539
/note="MIR2B repeat: matches 264..404 of consensus"
30402..30615
/note="MIR2A repeat: matches 264..453 of consensus"
<30801..>31136
/note="match: 5' EST AA256902 clone 682136"
30980..31222
/note="MERB repeat: matches 199..431 of consensus"
31232..31528
/note="Alusq repeat: matches 299..1 of consensus"
31530..31654
/note="MER4B repeat: matches 417..540 of consensus"
31836..32135
/note="Aluy repeat: matches 300..1 of consensus"
32200..32301
/note="Aluo repeat: matches 186..287 of consensus;
incomplete repeat"
32365..32493
/note="MIR repeat: matches 206..67 of consensus"
32883..33399
/note="MIR repeat: matches 77..196 of consensus"
33408..33667
/note="Aluy repeat: matches 1..291 of consensus"
33956..34043
/note="MIR repeat: matches 80..167 of consensus"
34725..34904
/note="Aluo repeat: matches 299..127 of consensus;
incomplete repeat"
34907..35207
/note="Aluy repeat: matches 300..1 of consensus"
35212..35344
/note="Aluub repeat: matches 133..1 of consensus;
incomplete repeat"
36545..36842
/note="Aluub repeat: matches 299..1 of consensus"
38190..38379
/note="MER3 repeat: matches 209..13 of consensus"
38382..38682
/note="Alusx repeat: matches 1..302 of consensus"
38836..38968
/note="MIR2 repeat: matches 145..2 of consensus"
38963..39279
/note="Aluub repeat: matches 3..296 of consensus"
39418..39773
/note="THE1A repeat: matches 354..2 of consensus"
39775..40120
/note="THE1B-INTERNAL repeat: matches 1580..1234 of
consensus"
40757..41023
/note="Aluo repeat: matches 37..301 of consensus;
incomplete repeat"
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Db 12722 AAAAATGTTGATATATTTAAAGCTTAATAGCCTCCTGACTACTGTTTAAAAAACAGTT 12781
QY 19107 tatgtcaagtgatataagaagaagtaaaatatacttttggtaaaagattagaagagcg 19166
Db 12782 TATGTCAAGAGTATATAGAAAGTAAGTAGTACCTTTAGTAAAAAGATTATAAGGGCC 12841
QY 19167 atagaatgtgacttttaccatcataaaggttaaaaaaatatctgttttgaagttc 19226
Db 12842 ATAAAAACGTGGATTTTACCTACATTAAGGTTAAAAAATATGTTTT----- 12893
QY 19227 aagcaagttttaaatgttaaatgtaaaaaaatctgtgtgttaaaactaatagctaaa 19286
Db 12893 --AAAAGTTTAAACCTTATTTGT-AAAGAAATTTGTGTGAACATATTAAGCTAAA 12949
QY 19287 gataaaaaggatcatccagttttctgtgactgagcatlaaagtaaaaaatgcaacagg 19346
Db 12950 GTTAAAAAGGTATCATCCATTTTCTGTGACTAGACATTAAGTAAAAATGCAACAGG 13009
QY 19347 ttttcttgaagcacaacctgtctttaaacaanaattataaaggtttaaaagagtcg 19406
Db 13010 TTTTCTTAAAGCATCACTGCTTTTAACAAAAATTTATAAAAAGTTAAAAAGAGCTA 13069
QY 19407 taaaaactaaccttatgtgtcaacaagaanaattgataaatagtctatgaggtttat 19466
Db 13070 TAAAACTTACCTTATGTGTCAAAACATAAAAAATTAGATAATATGTCTACAGGTTTAT 13129
QY 19467 taaaatlaagtttaacaataatacaacacataataaaggtaaaatttagcttatctgtc 19526
Db 13130 TAAATTTAAGTTTAACTTAACTTAAACACCCATAATATAAAAGTAAATTTAATCTAGCTGT 13189
QY 19527 ataaaaatcatacaagaagatatataataaalygtttagctttcttctgtccta 19586
Db 13190 ATAAAAATCATACAGACAGCATTTTAAATATTAATTAAGTTTAACTTCTTGGTCTA 13249
QY 19587 aaaaactaat-aaaaataggtccctaagaagaacttacttactagaagtcataagagt 19645
Db 13250 AAAACTTAATAAAAATAGATGATPAAAAAACAATCTATTTACTAGAGATCATAGAAGT 13309
QY 19646 taaagacttaaaacaacttggcaattlaagaagcatacaagatgcaaatgcctgtc 19705
Db 13310 TAAAGACTTAAACAACCTTGGCAATTAGAGGGCATACCAAGATGCAAAATGCTGTGT 13369
QY 19706 gaaaatgatacaatattccatctgcacattaaacaagaagctgttatagtctgtgcaca 19765
Db 13370 GAATATGATCAAAATATTCATCTGCAAGTATA-AAAAACAATGTATGCTGTGCACA 13428
QY 19766 tggcagggccagagggccctcatgtccccccttcaactaaagtgttccctcagttcacacagg 19825
Db 13429 TGGCAGGCCAGAGGCCCGCGATTGTCCCCCTTCCACTAAGTGGTCCCTCCAGTCCACCAGG 13488
QY 19826 cgttggcctgcatgtagctcttttccagagttctacagccttggagtaataagtcatagcc 19885
Db 13489 CGTGGCTGATGTAGTCTCTTTCCAGAGTCTACAGCCTAGATTAATAGTCATGCCA 13548
QY 19886 aactcctctgtcfa-----ttccctgtgtgtagcccccgagggtccatccagctc 19935
Db 13549 AGCTCTCTGTGCTATATCCCGAAATCCCTGTCAAGTCAAGCCCAAGGCCATCCAGCTTC 13608
QY 19936 cgtctccacaactaaagttactactatgtctccacacagagagaaactta 19988
Db 13609 CGTCTCCCAACATAAGTTCACTCTGTGTCTCATGCGCAGGAGGAGACTTA 13661

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2000, 20:12:08 : Search time 21727.1 Seconds
(without alignments)
-3493.772 Million cell updates/sec

Title: US-09-339-352-8_COPY_1_25000
Perfect score: 25000
Sequence: 1 aggaaccttcacagaggaac.....cttcacatcttgcaatacca 25000

Scoring table: IDENTITY_NUC

Searched: 821193 seqs, -1518192014 residues

Database: GenEmbl:*

Word size: 0

Number of hits that pass the threshold: 1642386

1: gb_bal:*
2: gb_ba2:*
3: gb_com:*
4: gb_ov:*
5: gb_pat:*
6: gb_ph:*
7: gb_pl1:*
8: gb_pl2:*
9: gb_pl1:*
10: gb_pr2:*
11: gb_pr3:*
12: gb_ro:*
13: gb_sts:*
14: gb_sy:*
15: gb_un:*
16: gb_y1:*
17: em_fun:*
18: em_hum1:*
19: em_hum2:*
20: em_in:*
21: em_com:*
22: em_or:*
23: em_ov:*
24: em_pat:*
25: em_ph:*
26: em_pl:*
27: em_ro:*
28: em_sts:*
29: em_sy:*
30: em_un:*
31: em_v1:*
32: gb_htg1:*
33: gb_htg2:*
34: gb_in1:*
35: gb_in2:*
36: gb_ba1:*
37: em_ba2:*
38: em_hum3:*
39: em_hum4:*
40: gb_pr4:*
41: gb_htg3:*
42: gb_htg4:*
43: gb_htg5:*
44: gb_htg6:*
45: gb_htg7:*
46: em_htg1:*
47: em_htg2:*
48: em_htg3:*
49: em_hum5:*

50: gb_pl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	25000	100.0	102258	11	HS295C6	297876 Human DNA s
2	1700.4	6.8	78661	11	AC005350	AC005350 Homo sapi
3	1675.4	6.7	149566	11	AC003081	AC003081 Human BAC
4	1670.2	6.7	212118	44	AC009264	AC009264 Homo sapi
5	1659.8	6.6	152794	44	AC009794	AC009794 Homo sapi
6	1592.6	6.4	192151	33	AC007282	AC007282 Homo sapi
7	1574.8	6.3	220218	40	AC006288	AC006288 Homo sapi
8	1563	6.3	94320	10	AC002564	AC002564 Human BAC
9	1558.6	6.2	73029	11	HSBA329J7	AL118497 Human DNA
10	1548.2	6.2	161326	11	AC004067	AC004067 Homo sapi
11	1546.2	6.2	110401	11	AC004068	AC004068 Homo sapi
12	1541	6.2	181883	44	AC016735	AC016735 Homo sapi
13	1533.2	6.1	118205	32	HSBJ149L1	AL022401 Homo sapi
14	1528.4	6.1	206784	11	HS9317	AL022401 Homo sapi
15	1524.2	6.1	144159	43	AC015692	AC015692 Homo sapi
16	1521.4	6.1	151834	40	AC005399	AC005399 Homo sapi
17	1519.6	6.1	184490	11	HSB2828	U82828 Homo sapien
18	1519.2	6.1	163712	11	AC004065	AC004065 Homo sapi
19	1517.6	6.1	292721	40	AF130343	AF130343 Homo sapi
20	1515.8	6.1	182865	43	AC011330	AC011330 Homo sapi
21	1514.4	6.1	126149	40	AC006352	AC006352 Homo sapi
22	1514	6.1	119580	10	AP000466	AP000466 Homo sapi
23	1512.8	6.1	117954	10	HSAC002065	AC002065 Human BAC
24	1511.4	6.0	148800	33	AC007028	AC007028 Homo sapi
25	1511.2	6.0	167171	33	AC006269	AC006269 Homo sapi
26	1508.4	6.0	166219	11	AC003084	AC003084 Human BAC
27	1507.6	6.0	186324	41	AC009405	AC009405 Homo sapi
28	1507.4	6.0	152393	41	AC010682	AC010682 Homo sapi
29	1502.4	6.0	156929	41	AC009277	AC009277 Homo sapi
30	1501.6	6.0	181751	42	AC008784	AC008784 Homo sapi
31	1500	6.0	143119	11	AC011059	AC011059 Homo sapi
32	1499.4	6.0	140167	11	AC004010	AC004010 Human BAC
33	1497.4	6.0	170208	32	CNS01DUA	AL133233 Homo sapi
34	1496.4	6.0	170967	40	AC005023	AC005023 Homo sapi
35	1495.6	6.0	143427	10	AC002432	AC002432 Human BAC
36	1494.2	6.0	136968	32	HS668J24	AL034346 Homo sapi
37	1493.6	6.0	141773	32	HS107G16	AL121980 Homo sapi
38	1492.6	6.0	194000	33	AC000016	AC000016 Homo sapi
39	1492.6	6.0	128000	33	AC004046	AC004046 Homo sapi
40	1487.4	5.9	98770	11	HS36411	AL031319 Human DNA
41	1486.8	5.9	125290	40	AC004986	AC004986 Homo sapi
42	1484.4	5.9	192548	40	AC005296	AC005296 Homo sapi
43	1483	5.9	175463	43	AC007272	AC007272 Homo sapi
44	1482.4	5.9	198363	44	AC013545	AC013545 Homo sapi
45	1482.2	5.9	172383	45	AC008065	AC008065 Homo sapi

ALIGNMENTS

RESULT 1
HS295C6 HS295C6 102258 bp DNA
LOCUS Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains
DEFINITION ESTs, CA repeat, STRs and Cpg island.
ACCESSION 297876
VERSION 297876.1 GI:2582745
KEYWORDS 1q24; Cpg island; repeat polymorphism.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 102258)
AUTHORS Grafham,D.
TITLE Direct Submission
JOURNAL Submitted (27-OCT-1997) Chromosome 1 Project Group
(http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Nov 2, 1997 this sequence version replaced g1:2465042.
IMPORTANT: This sequence is the entire insert of clone 295C6.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variations annotated may not be found in the sequence submission
corresponding to the overlapping clone as we submit sequences with
only a small overlap as described above.
This sequence was generated from part of bacterial clone configs of
human chromosome 1, constructed by the Sanger Centre chromosome 1
mapping group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1/
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The true left end of clone 295C6 is at 1 in this sequence. The true
right end of clone 295C6 is at 102258.
295C6 is from the library RPC11 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/
Location/Qualifiers
1. .102258
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/db_xref="taxon:9606"
/chromosome="1"
/map="1q24"
/clone="RP1-295C6"
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891. .1180
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1375. .1683
/note="AluSP repeat: matches 303. .1 of consensus"
2028. .2310
/note="AluSq repeat: matches 300. .1 of consensus"
2612. .2903
/note="AluSq repeat: matches 301. .1 of consensus"
complement(4475. .4866)
/note="match: 223618 STS containing (CA) repeat"
4625. .4670
/note="23 copies of GT 100 & conserved; differs from
223618"
4766. .4897
/note="MIR2 repeat: matches 145. .1 of consensus"
4969. .5140
/note="MER42c repeat: matches 1475. .1300 of consensus"
5146. .5448
/note="AluJo repeat: matches 302. .1 of consensus"
5503. .5795
/note="AluSg repeat: matches 1. .299 of consensus"
5797. .3525
/note="MER42c repeat: matches 1265. .1124 of consensus"
5923. .6039
/note="L1MB6 repeat: matches 920. .804 of consensus"
6123. .6415
/note="AluSx repeat: matches 1. .292 of consensus"
7799. .8099
/note="AluSx repeat: matches 302. .1 of consensus"
9002. .9302
/note="AluSg repeat: matches 2. .303 of consensus"
9692. .9983
/note="AluJo repeat: matches 1. .301 of consensus"
10986. .11071
/note="MIR2 repeat: matches 146. .60 of consensus"

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/note="MIR repeat: matches 262. .70 of consensus"
repeat_region 12180. .12479
/note="AluSg repeat: matches 1. .300 of consensus"
repeat_region 13246. .13500
/note="MIR repeat: matches 256. .1 of consensus"
repeat_region 13907. .13973
/note="MIR repeat: matches 75. .141 of consensus"
repeat_region 13975. .14489
/note="MIR repeat: matches 526. .1 of consensus"
repeat_region 15702. .16064
/note="MIR repeat: matches 1. .371 of consensus"
repeat_region 16144. .16585
/note="MIR repeat: matches 9. .466 of consensus"
repeat_region 17173. .17534
/note="MIR repeat: matches 105. .449 of consensus"
prim_transcript <17766. .>18427
/note="match: multiple ESTs; match: AA165668 C16515
AA077391"
repeat_region 18004. .18120
/note="3 copies of 39 mer 81 & conserved"
prim_transcript 19377. .>21532
/note="match: multiple ESTs; match: N46026 H60052 H12822
T62974 AA283144; match: T57835 F00049 N75628 AA382351
AA300207; match: W57181 N52820 AA337499 W87891 H84729;
similar to endogenous retrovirus POL POLYPROTEIN"
prim_transcript <22156. .>22928
/note="match: multiple ESTs; match: AA401243 AA258918
AA248892 AA096209 R36280"
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/note="MIR repeat: matches 105. .449 of consensus"
repeat_region 24473. .24785
/note="AluSg repeat: matches 1. .299 of consensus"
repeat_region 25027. .25058
/note="16 copies of 2 mer 88 & conserved"
repeat_region 25877. .25987
/note="L1PA5 repeat: matches 788. .892 of consensus"
repeat_region 26022. .26312
/note="AluSP repeat: matches 1. .295 of consensus"
repeat_region 26752. .27050
/note="AluSg repeat: matches 1. .299 of consensus"
repeat_region 28012. .28312
/note="AluSg repeat: matches 1. .303 of consensus"
repeat_region 28316. .29066
/note="L1MB3a repeat: matches 109. .907 of consensus"
repeat_region 29517. .29629
/note="MIR repeat: matches 262. .151 of consensus"
repeat_region 29631. .29928
/note="AluY repeat: matches 1. .295 of consensus"
repeat_region 29937. .30237
/note="AluSg repeat: matches 1. .301 of consensus"
repeat_region 30238. .30315
/note="MIR repeat: matches 158. .76 of consensus"
repeat_region 31096. .31287
/note="MIR repeat: matches 56. .262 of consensus"
repeat_region 31289. .31379
/note="MIR repeat: matches 146. .56 of consensus"
repeat_region 31479. .31525
/note="MIR2 repeat: matches 146. .95 of consensus"
repeat_region 33069. .33318
/note="MIR repeat: matches 9. .253 of consensus"
repeat_region 35565. .35744
/note="MIR repeat: matches 262. .74 of consensus"
repeat_region 36165. .36466
/note="AluSx repeat: matches 1. .302 of consensus"
repeat_region 36692. .36944
/note="MIR repeat: matches 3. .240 of consensus"
repeat_region 36999. .37299
/note="AluSx repeat: matches 301. .1 of consensus"
repeat_region 37924. .38114
/note="L1MA2 repeat: matches 1055. .866 of consensus"

repeat_region 38108..38475
/note="MSTA repeat: matches 426..1 of consensus"
repeat_region 38479..38657
/note="LIM2 repeat: matches 874..687 of consensus"
repeat_region 38658..38957
/note="Alusg repeat: matches 300..1 of consensus"
repeat_region 38958..39580
/note="LIM3 repeat: matches 699..85 of consensus"
repeat_region 39385..39875
/note="Alusg repeat: matches 292..1 of consensus"
repeat_region 39877..39951
/note="LIM4 repeat: matches 88..14 of consensus"
repeat_region 39944..40919
/note="L1 repeat: matches 4416..5390 of consensus"
repeat_region 40769..41662
/note="L1P2 repeat: matches 1..893 of consensus"
repeat_region 41764..42556
/note="L1 repeat: matches 5133..4305 of consensus"
repeat_region 42557..42857
/note="Alu repeat: matches 1..301 of consensus"
repeat_region 42876..43925
/note="L1 repeat: matches 4313..3215 of consensus"
repeat_region 44235..44498
/note="MER43 repeat: matches 3..272 of consensus"
repeat_region 44788..44860
/note="MIR repeat: matches 154..82 of consensus"
repeat_region 44933..45220
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unsure 45304..45336
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repeat_region 45337..45637
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repeat_region 45934..46220
/note="Alu repeat: matches 302..14 of consensus"
repeat_region 46817..46935
/note="MIR repeat: matches 35..154 of consensus"
repeat_region 47393..47677
/note="Alusx repeat: matches 1..302 of consensus"
repeat_region 48309..48404
/note="MIR repeat: matches 48..140 of consensus"
repeat_region 48620..48862
/note="MER218 repeat: matches 347..102 of consensus"
repeat_region 48865..49159
/note="Alus repeat: matches 1..296 of consensus"
repeat_region 51182..51467

Query Match 100.0%; Score 25000; DB 11; Length 102258;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 25000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 aatgaagaacatcctcatgcatgataggaataatcatatcatgaaatggccat 120
Db 40021 AATGGAAGAATCTTCATGCTATGATGGAATAATCATATGAAATGGCCAT 40080

QY 121 tgcctaagtaattatagatcctatgcacatcccatcaagctaccatgacttct 180
Db 40081 TGCTCAAGGTATTTATGATTCATGCCATCCCATCAAGCTACCAATGATTTCT 40140

QY 181 cagaattgaaaaatctctttaagttcatatggaacaaaagaagctcattgta 240
Db 40141 CAGATTGGAAAAATCTACTTTAAAGTTCAATGGAACCAAAAAGAGCTGCATTGT 40200

QY 241 agataatcctaagcaaaagaagaagctgagagcatcatgcttactgcttcaact 300
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Db 40261 ACTACAAGGCTACATTAACCAAAAGCATGTGCTACTGATCCAAACAGAAATATG 40320

QY 361 aatggaatgaaacagatccctcagaataataaccacatctacaaacatctgact 420
Db 40321 AATGGATGGAACAGATCCCTTGAATAATATCCACACATCTACAAACCATGAT 40380

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QY 601 aagaacctaggaatccatccatcagtagacatggtgcaaggacttcactga 660
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QY 721 ctctgaaacagaagaataatcatcagatgtagacaggaatccttaagaatg 780
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D	41461	AACACTTAGACACAGAGGTGGGAACTACACACACAGGCCCTGTGTGGCTGGGGGAA	41520
Q	1561	gggggagggatagcatlaagagataacctaatgttaaaagatgaatlaaggtgcagca	1620
D	41521	GGGGGGGAGATAGCATTTAGAGATATACCTATGTAAGAGATGAAGTAAATGGGTACACA	41580
Q	1621	taccacaatagggaacatgtataataacgttaaacaaacctgcacattgtgcacatgaacct	1680
D	41581	TACCAACAAGGAGACATGTTACATTAACGTAACCAACCTGCACATTTGTGCATGTACCT	41640
Q	1681	aggaacttaagtatataataaataataataataataataaataaagaattaaaaaac	1740
D	41641	AGAACTTAAAGAT	41700
Q	1741	tcatcaatgaacataattttttatcatgataaataattctaaaaaataaaacacttgat	1800
D	41701	TCATCAATGAACATAATTTTATATCGATGAATATATCTATAAAAAAACAACACTTGAT	41760
Q	1801	gtatccaactgtccactttttgtcttggtgtgcctgtgtgtgtgtgtgtgtgtgtgtgtgtgt	1860
D	41761	GTTATCCCATCTGTCACATTTTGTGTTGCTTGCCTGTGGGGATATCTCAAGAA	41820
Q	1861	accttggccactccaatgtcctcttgagagatcccccacagtttctcttgtagagttcat	1920
D	41821	ATCTTGTGGCCACATCCAAATGCTTGAAGATCCCAAAATGTTCTTGATGAGTTTCTAT	41880
Q	1921	ggttgatgtctcaaatgcatctttgaacttgaatttttgataagaagaataagatgc	1980
D	41881	GGTTGATGTCTCAAAAGTCCATTTTGACTGATTTTGTATATACCAAGATATAGAGTTC	41940
Q	1981	tagttcattcalctgcagataagataccagtttccacacaaattatgaaggatc	2040
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Q	2041	gaccttcccttatattctcttgaccttcttggctcaaaaataagttcacatgatagtatag	2100
D	42001	GCTTGTTCCTTATATCTTGAGCTCTTGTGTGAAAAATTAAGTCACTGATGATGATGAG	42060
Q	2101	ttctattctctgttctctatctctgtccacatgctcatgtctgttcttcagcgcaatc	2160
D	42061	TTTATTTCTGTGTTCTCTATCTGTCTCCACGTGTATGTCTGTCTTTTCATGCCAGTAC	42120
Q	2161	tatgcatttgggtgtgctatagcgtggtatataattgaagtcagataabatgatattccctc	2220
D	42121	TATGCAATTTGGGTGCTATGATCTGAGTATATTTGAAGTCAGATATATATATCTTCC	42180
Q	2221	taattatctcttggcttgcagaatgcttggctctctcgtggctcttggcttggcttgcagt	2280
D	42181	TGATTTATCTTTTGTGCTCAATAGCTTTGTGCTACTCTGGGTCTTGTGTGCTCATGT	42240
Q	2281	aaatttgaatatttttttcttctattcttgcataagaatgctatggtattgttlaagta	2340
D	42241	AAATTTTGAATTTTTTTTTTTCTATTTCGTGAAGATGCTATGATTTTGTTAGTA	42300
Q	2341	ttgcattgaactcttagatgtcttgggtagtagaacaattcccaactataaagcatg	2400
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Q	2401	gaatacttctaatttttttttggggccctccaactcttgtaacaattttagt	2460
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Q	2461	ttcaaggttagaatcttccaactcttggtaataactagacacttaattattatttag	2520
D	42421	TTCAGGTAGAGATCTTTACTCTTTGGTAAATTAAGTAGACTTTATTTATTTTAG	42480
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Dd	42481	CTATGTTAAACAGATTACTTTCCTTGATTCTTTTTCAGATGTCTCCGTAGCATATA	42550
Qy	2581	gaatagccggaattcttbyggccggcgcgylgtgtcaagccctgtaatcccaagcacttbyga	2640
Dd	42541	GAATAGTGTATTTTGGCCGGGCGGGTGCGTCAAGCTGTAAATCCAGCACTTTGGGA	42600
Qy	2641	ggcgaagccggcgcgatcaagaggtcgaagagatcgagacatcccggttaacacggtga	2700
Dd	42601	GGCCAGGCGGGCGGATACGAGGTCAGAGATTCAGACCACTCGGTAAACGCGTAA	42660
Qy	2701	acctggtctctatbaaacaacaaaatlaacggggcggtgtgtgcggcgccctgtgtc	2760
Dd	42661	ACCTGCTCTCTATTAATAACACAAAATTAAGCGGGCGCTGTGGCGGGCGCTTGCTC	42720
Qy	2761	ccagctactcaagagcgctcgagcgaggaataagatgaaccggggagcgagcgctgcag	2820
Dd	42721	CCAGCTACTCAGAGAGCGTCGAGGCAAGAAATATGATGTAACCGGGAGGCGCTGCAG	42780
Qy	2821	tgaagcgaagacagcgcaactgcagtcgaagccctggcgaaagagggagactccgtctcaa	2880
Dd	42781	TGAGCGGAGACAGGCCCACTGCAGTCCAGCCGCGGCGAAAGGAGAGCACTCCGTCAAA	42840
Qy	2881	aaaaaaaaaaaaaaaaaagaaagaaagaaagaaatgctgattcttggatgatgtattgcat	2940
Dd	42841	AAAAAAAAAAAAAGAAAAAGAAAAAGAAAGTGTGATTTTGTATGATGATTTTGTAT	42900
Qy	2941	actgtgaccttgatgaatttgatgtgaatcgaatctaaatgtgttcttggtgagcccttaag	3000
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Qy	3001	ttcttcaaatataaataagatcatctcgaaacaaggaataatttgactcttcccttccaat	3060
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Qy	3061	ttgatgtccattctcttctctctctgtctgtatcatagaagactccagttatagtgtga	3120
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Qy	3181	ctccctatcatatgaatactgaatgtgtcgtgtcatctcataatgagcttctctatgtag	3240
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Qy	3241	gtatgtccctctatacaacagttcttbyggaatttatacatgaagagatgttgaatttc	3300
Dd	43201	GTATGTTCCTCTCTATACACAGTTTTTGGGAATTTTATCATGAAGGAGTGTGAATTTT	43260
Qy	3301	atcaactcgtctttagagatacaactcgaagaatgaataatgattgttctgtcttcaattctga	3360
Dd	43261	ATCAACTGCTTTTTCAGATCACTGAAGTAATGATATAGGTTTTGTCTTCATTCTGTA	43320
Qy	3361	gataagacatatcacagtgatttgatattgcataatgccaaccacttgatccctggagat	3420
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Qy	3421	aaatcccaactgatacgaatggaatgatacttttaataatgtgttgaaccagttgtcga	3480
Dd	43381	AAATCCCACTGTATATATATGATATATCTTTTAAATATGTTGTGAACCAATTTTGCTAG	43440
Qy	3481	tatttgcgtcgaagatttatacaaatatgaatgaactgaagaaactggccgtgaactcttc	3540
Dd	43441	TATTTTGCTGAGGATTTTACATCAATTTCTCAAGAAATACCTGGCGTGTAGCTTTCTTT	43500
Qy	3541	tttttgaatgactttgtctgtgttlttgatcaaggtlaaactgagccctgttgaatgagtt	3600
Dd	43501	TTTTGATGTAGACTTTGTCTGGTTTTGATATCAGGGTATATACGGCCTGTGAATAGAGTT	43560
Qy	3601	tggaaatattccctccctctctatgttctcaagaatgatttgagtaacggtgtatattagttc	3660
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D	b	45841	TAAATGCCTAGAAGGTCCCGGTTTCATGTAATTTATCTTTTTTAAAAAGATTAAAT	45900
OY	5941	aatttcattaaccaaagtgttaatttttccctttctttttttttttttaagaacg	6000	
D	b	45901	AATTTCTAATTAACAAGATGCTAATTTTTTTCTTTCTTTTTTTTTTTTAAAGAACG	45960
OY	6001	ggcttgctctgcccaagsgcttggaagtcaggtagcatctcgctaacgcgaacc	6060	
D	b	45961	GGTGTTGCTGTGTCCCAAGSGTGGAGTSCATGAGGCAATCCGGCTCAGCAAGCTC	46020
OY	6061	cgtctccttgtcaagtatcctctcaectcaagctcccagtagctgggcttaacagca	6120	
D	b	46021	CGTCTCCTTGCCAGAGTATCCTCTCACCTCACCCTCCCTAGTACGTGGGCTACAGCA	46080
OY	6121	cgtagccacaaccaactaatltttgatatlttbtgagaagaggttttgcatgtgt	6180	
D	b	46081	CGTGCCACCAACCACAACTAATTTTTGTATTTTTGTGGAGAGAGGTTTTCGCAATGTT	46140
OY	6181	ccaagctggtcttgaaacctctgtggtccaagtatcacacctgtctggtctcccaagtgc	6240	
D	b	46141	CCAGCGCTGGTCTTGAAGCTCCTGGGCTCAAGTATGCACCTGTCTGGGCTCCCAAAGTGC	46200
OY	6241	tgggatccaggaatgaagccctggccttgatlttccaataaaaatcatccaataaata	6300	
D	b	46201	TGGGATTACAGGCAGACACCTGGCCTTGATTTTTTCAAAAATAATATTCACAAATAAAAT	46260
OY	6301	aaaaactcttcaagacatgtatctatgatttgccttggaagaagacacgtatc	6360	
D	b	46261	AAAACTCTGCGACACTATGATTTCTGAGTTTGGCTTGGAAAAAGGACTACGGTATC	46320
OY	6361	tttaagacctctctcttcttgggttcagggtctgttbtgttaaagtctgt	6420	
D	b	46321	TTTAAAGACTCTCTCTCTTTGGGTTCAAGSGTCTGGTTTGGTAAAGTTGTAAGAAGTTGT	46380
OY	6421	cttggcttatlttccaacctcttaagctgtacctctccaaggtaaacatltttccta	6480	
D	b	46381	CTTTGGCTTATATTCCAACCCCTTTAAGCTGATCCCTTCACCAAGGTAACATTTTTCCTA	46440
OY	6481	cctggaatttccccagtgactacaagagtcacactatacttcattgtccaaagacttgt	6540	
D	b	46441	CCTGGAAATTTTCCCAGTACTACAGAGTCCACTTTATTTTCCATTGCTTAAAGACCTTGT	46500
OY	6541	tttcaacctgttgcattaaagaacataatgtatatactctctgagaatgtgcgcgg	6600	
D	b	46501	TTTTCACTGGTTGCAATTAAAGAACCATATATATATTATATCTTGAGAAATGGCTGGGG	46560
OY	6601	agaatggggtgacttttttaagcttcaaaagccatgaagaagtcgaatgcaagcacta	6660	
D	b	46561	AGAAATGGGTCACCTTTTAAAGCTTCAAAAGCCATGAAGATCAAGCAATGCAGGCACATA	46620
OY	6661	gggtgaatgatttacaatggtcgtgaaggtgycgaaggtgcatctcgtacccctccaatt	6720	
D	b	46621	GGGGTAAATGTTTTTAACAATGGCTTAAGGTGAAGTGGCAGGGTCAATTCGTATACCTCTCAAT	46680
OY	6721	cactcatagaagcagctacccaactggaagcccttbttaaaagattctctccaagac	6780	
D	b	46681	CACCTTATGAAGGCGACTACCCACTGAGCAGGCCCTTTGTTACAAAGATTTCTCCAGGAC	46740
OY	6781	acaacagcattttgatygnactaaatlataaagcagcgcatatataagaygttgatagc	6840	
D	b	46741	ACAACAGCATTTTGAATGGGACTAAGTATTTAAAGCAGCATATATTAGAGAGGTGGATAGC	46800
OY	6841	ctgtgcaaaaatctgtagaagtcagatagacaaaggtccaabctcagctatacttttac	6900	
D	b	46801	CTGTGCAAAAATTTGTAGAAGTCAAGTATTAACCCAGGSTCCAAAATCTTAGCTATATCTTTTAC	46860
OY	6901	ttgacaacctcaagaaagctgttagtgtctcttgggtctcagtttctcaatgcatataa	6960	

D	46861	TTACAACTCGTAGGAAAGCGCTAGTGGTTCTCTGGGCTCAGTTTTCTCATCATATAA	46923
Q	6961	atgagataaaaaatactaccaggacgtgtaaagaataatactagaactagcaagvtga	7020
D	46921	ATGAGGATTAATAATATCTACCCAGAGCATGTAAAGATATAATATCATGACGACTACAGGTGA	46980
Q	7021	ctggacattgtggaatgtaagaagatagttataattcaatggaataataattggaag	7080
D	46981	CTGGCATATGGGATGGATGAAGATAGTTATAATTCACATGGAAATATAATTTTGAAG	47040
Q	7081	aacccaagattaaagagaataaaaaagagaaataattggaggvtggagtgctaagatatt	7140
D	47041	AACCAAGATTAGAGAAATATAAAGAGAAATAATGGAGGGGTGAGGTACCTCAGACTATT	47100
Q	7141	ctaattaccgtcatctgttaaatctcaaaaactaaagactaatgcaatgcaatgtgaga	7200
D	47101	CTAATTTACCTGCTATGTGTAAATCTAAAACTTAAGAGCTAAATGCAATTACTGTGGAAA	47160
Q	7201	tagtgtaccaatggttcataccacttgaagctctcttcgcgtgtggtcaatagaaaggtgc	7260
D	47161	TAGGTACCAATGTTTCATCCACTTGAAGCTTTCTTGCTATGTGGCATATAGAAAGGCTC	472220
Q	7261	ccgcattgtctataatgtcttgcaacagctcccaatttgcgcaattalataagccaagcag	7320
D	47221	CCGCATGTTCTTATATAGTGTGCACAGCGCTCCCATTTGCCAATTAATATAGCAACGCGAG	47280
Q	7321	tcctttttatggccgtgtgtcaatatataatgaataatgatctcttggaaagtattg	7380
D	47281	TCTTATTTATGGCTGTGTCTATATTAATATATGATATATATATCTCTTGAAGATATG	47340
Q	7381	agatttgacaatgtaatttcacagctcacccataatagaatgtcttttaggcctcagt	7440
D	47341	AGATTTGAAATGATGATTTTCACAGTCCACTCATATATAGAAATGTCTTTTAGGCTCAGT	47400
Q	7441	gtgtgtgctcatgcccataatccagcacctgtggagggvtgagcgcgagcaattcttga	7500
D	47401	GTGTGCGCTCATGCCCATTAATCCAGCACTGTGGAGGGGTGAGCGGCGAGATTTCTTGA	47460
Q	7501	gtctaggaatttgagatacagtcagtcagccaatagtggaagctccactctcaataaaatcc	7560
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Q	7561	aaaaagcttagctgggtgtgtgtggcactgtggagagctgaagcagagagattgctgaac	7620
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Q	7621	ccggagagcgagaggtgtgcagtgaagccaagatcatgctctgcaactcagcctggvtgaca	7680
D	47581	CCGGAGGCGGAGGTTGCGAGTGAAGCCAGCATCATCTGTGTGACATTCAGCCGTGGGTGACA	47640
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D	47701	TGGAACTATTTACTATTTACTATGATGCTGTGTTTTTTTTCTTAAATCTTAAATATTC	47760
Q	7801	agcgttccagaatcccttgacatcccccagaagccagtaattcaatttggaaatactgctt	7860
D	47761	AGCTTCCAGATCCTGTGACATCCCAAAAGCCAGTAAATTCATTTTGAAAAATACCTGCTT	47820
Q	7861	caaaatgtcttcacatcacatacttttgttaggacatctccagttcaagatcaaggttcag	7920
D	47821	CAAAATGCTTTTCATCACATACTTTTGTAGGAGACATCTCCAGTTTCAGATTCAGGCTTCAG	47880
Q	7921	cgtgcatagcagcctcaggaggtctaaagaagcagaagaggvtgcaggctcagagaaggt	7980
D	47881	CGTGCAATCAAGCCTCAAGAGGTTCTTAAGAGGACAGAGAGGAGGTCCAGGCTCAGAGAGG	47940
Q	7981	aagtttgctctgcagtgctagtgtgaggaagagctcccaagctccattctcttggcagtg	8040
D	47941	AAGTTTGCTCTGCACTGCTCTAGTGAAGAGAGGCTCCCACTGCTCTTCTTTGGGCAGTG	48000

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OY	800.1	ggcctctctgtcccttaacagttgttcagagacctctggacacctaaagggctgaaggcca	4806.0
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OY	4812.1	gctcaaaacctgttccaactacatgaacgctttggaacttagagattccactctg	4818.0
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OY	4818.1	aacttggttagaactattgcccacagagatgaggaaacaacatgaggaaatgaaga	4824.0
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QY	9181	tcaaaaaaanaaaaaaagaatctgcatctgcagatctatgtgtcctcaagtcaagcgctg	9240
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QY	9241	aagaaecccttataagaagtlaccatbaagaccagagatgycatagtaagctcaag	9300
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QY	9301	gagtggtgaatgctataaggtcttcctccatcctcttgagctctcgaagttcttgagct	9366
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QY	9361	tctcgtacataatgtcttataagctctcccaactcccaaccacactgctattgtgcttg	9420
Db	49321	TTCCGATCAATGTTGTGTACAGTCTCCCACTCCCAACCCCACTGCTATTGTGGCTTG	9438
QY	9421	taaaagtacagctctctcatttgaacatctaaatctccaactctgacataatgtg	9480
Db	49381	TAAAGTACACTCTCTCATTTGTGTAACATCTAAATCTCCAACTGTAACATAAATGTG	9494
QY	9481	agaagaatgtattcaagaatgtcttcgtgattctcactgtgatggagtttcaagagag	9540
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QY	9541	ggtaaagtacaaagtctcaagatcagatcgttaabataatgatgcttatgacatccagtgaag	9600
Db	49501	GGTAAGTAGCTAAAGTTCACATACGTAAATATTAGATGCCATTGTGACATCCAGTGAGAG	9656
QY	9601	tgcgccatagtgtaggtcattgtttgttttatagaattcagggcaaaaatctgctcta	9660
Db	49561	TCGCCATAGGTAGCGGATTTGTTGTTTATGTAATTCAGGACAAAAATCTGTCTCTA	9682
QY	9661	gaattcaggaacaaaagactcaagcgaatctcgtgtcttgatgctctagaactcgggtgagt	9720
Db	49621	GAATTCAAGGACAAAAGACTGAACGAAATTCGTGCTGATGCTGAGACTGGGGTAGGT	9686
QY	9721	aagcaacttcgaggaactctgaagatgaagtgtctgtcttaagttttgtatacagctcttc	9780
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QY	9781	actgctccatcattaccatcatatgaaggttaagacgaataaaatgttcaactaagaagatga	9840
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QY	9841	gtagaagaagactagaaggttcaaaagacagataccgtgaagtcacacaaatltaaagatgta	9900
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QY	9901	aagaaactaagcgaagaagactgaataatagtgatattgaagcgttaaaagcgaacatga	9966
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QY	10021	aagctatgttcaaccatctgtgtatgggtctgaagaagaaggtacactgtttgtggcaata	1008
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QY	10201	atcaatttatttgtatgataataataaagggagacatgaagcgagttataataactt	1026

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Dd	50221	TACAGATTACTTTTCCTAGAAAGTTTATTGGTAAAGTTAGGGGGAAGCAGCACGGA	50280
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Qy	10741	aactcttgaagtgtaattctcttagcagaagaagtagtctcctttagactgaagtgatt	10800
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Dd	51181	ATCAGGCCCTGTAATCTTAGCACTTTGGAGGCTGAGGTGGCAGATTTGCTTAAGCTCAGG	51240
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Dd	51301	AAAAAAAAATTAGCCAGCGTGTAAGTGCACATGTCTGTGGTCCCACTTCTCAGAGGGCTG	51360d
Oy	11401	tgttgtgaagaatcgcgttgagacttggaaattgaagttgaagtgaagtcagatcatcgcac	11460o
Dd	51361	TGGTGGAGAAATCGCTTGAAGACTGGGAATTGAAGTGAAGTAGACTGAGATCATGCCAC	51420d
Oy	11461	ctcactccccacttgygtgacagagtgaagatccalcacaanaaaatatatatatgt	11520o
Dd	51421	CTCACTCCCCACTGGGTGACAGAGTAAGAATTCATCTCAAAAAAATAATATATATAGT	51480d
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Dd	51481	AATATATATATAGAGAGACAGAGATATGTTGTTGGAATGTACGAAGAGATAGGAAG	51540d
Oy	11581	catacgaagtgctaacagagatgtgtgtgacaacatcgcgttgcgaactcctgtgtc	11640o
Dd	51541	CATCAGCGCAGTCTTAACCAAGATGTGTGTACAAACATCGCGCTGGCAACTCTTGTGTG	51600d
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Dd	52021	TCTCGAACATTCCTAACTGAATGGACCAAGTGGGAAACTGGTGCACTTCAATTAAGTGC	52080d
Oy	12121	tttaactagtcatagtgtttgaccaaatgttaattcctgtgtttgataatttgaagctt	12180o
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VERSION	AC005350.1 GI:3366562
KEYWORDS	HTG.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 78661) Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Kadner,K., Miguel,T., Miller,C., Pfluck,S., Pollard,M., Rojeski,H., Sudramanian,S. and Martin,C.H.
TITLE	Sequencing of human chromosome 5
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 78661) Ricke,D.O.
AUTHORS	Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 78661) Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M., Davis,C.A., Kadner,K., Miguel,T., Pfluck,S., Pollard,M., Rojeski,H., Sudramanian,S. and Martin,C.H.
TITLE	Direct Submission
JOURNAL	Submitted (31-JUL-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A.
COMMENT	Sequence submitted by: DOE Joint Genome Institute.
FEATURES	Location/Qualifiers

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Best Local Similarity 80.88; Pred. No. 1.3e-284;
Matches 2248; Conservative 0; Mismatches 341; Indels 193; Gaps 15;
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Db 12482 AGGACCTTCAAGAGAACACCAACACGCTCAAGAAATTAAGAGATGCAACACA 12423
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QY 61 aatgaagaacatccatgcctcatgtagaagaatacaatatacgaataatgacatac 120
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Db 12422 AATGGAAGAACATTCCTGCTCATGCTAGGAGGAACAATATGTAANAATGGCCATAC 12263
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QY 121 tgcctaagtaattatagattccatgcatcccatcaagctaccaaagtacttcttca 180
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QY 181 cagaattggaanaactactttaaagtcatatggaaccaaagaagcctgcatgtcga 240
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Db 12302 CAGAAATGGAANAACATCTTAAGTTCAATGGAACCAAAAAGAGCCCGCATCGCA 12243
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Qy	361	aatgtaaaatggaacagatacccttcagaataataatcacacacatctcaaacatctgcactttg	420
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Qy	481	aaaactggtcagccatagttagaagaactgaaactgtaactcccttcctccactatacaa	540
Db	12002	AAAATGCTCTACCCATATGTATAAAGACTGAAACTGGATCCCTTCCCTTACACTTATACAA	119433
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D	10664	TTTTTTTCCCATAGAGTTGTTGAGCTCTCTCTCATATATGCTATAGCCCTTGTGCA	10625
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D	10504	TGCTTATGCTTGTGAGATTAATCTCAGAAATTTTGGCAATTTAATGTCTCTGAGAGA	10445
O	1891	ctccccaatgttttctttagtagtltcaatgttgaatgttcaaa-----t	1938
D	10444	TTCCCCAAATTTTCTTTTGTGAGTTCAATATGTTGAGGCTTATAGGCTTAAGTCTTGAT	10385
O	1939	ccaattgactgattcttctgatatagcaagagataggagctagttcatctatcatctgca	1998
D	10384	ACATTTTATTTGATTTTGTATGTGGAGAGATAGGGGCTTAGTTTCATCTTCTGCA	10325
O	1999	tatgatatccaagtttcccgagccaattttigaagsgattgtcttcccttatatc--	2057
D	10334	TATGGAATTCAGAGTTTCTTGAAACCAATTAATGAAGAGCAATCTCTCCCTAATGTGT	10265
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O	2116	tcatctctgtccacatggtctcatgtctgtctgttcaatgccaagtaactatgctattgggt	2175
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D	10144	ACTATGCGCTGTGATTAATATTGAAGTCAGAGTAACATAAATCCCTCGATTTGTGTTCTT	10086
O	2234	ttgcttcagaagctcttggtcctactctgggtcttctgtgttccatgtataatlttaga	2293
D	10085	TTTGTCAGAGTAAGCTGTACATATCTCTGGGCTTTTGTGGTTCCAAATATATTTTAAAGA-T	10027

[illegible]

<http://www.nhgrl.nih.gov/DIR/CTB/CHR7> or send
mailto:egreen@nhgrl.nih.gov

SOURCE INFORMATION: Clones R0009H02 is from the first release of the human BAC library CTR-97SK-B. The library contains cloned DNA from the male fibroblast cell line 97SK. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8754-7 (1992); U-J. Kim et al., Genomics 34:213 (1996). This clone is available from Research Genetics, Inc. (<http://www.resgen.com>).
VECTOR: pveloBAC11
selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:
The actual start of this clone is at base position 1 of RG009H02;
The actual end is at 149566 of RG009H02. The orientation of this clone
is unknown.

This clone contains STS SWSS1764 (MID:g1254731).

FEATURES

Source

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Matches 2914; Conservative 0; Mismatches 726; Indels 553; Gaps 25;

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QY 61 aatggaagaacatcctcatgtctcatgataagaaatcaatcatgaaatgagcatatc 120
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* 16095 17002: contig of 908 bp in length
* 17003 17084: contig of 82 bp in length
* 17085 18593: contig of 1509 bp in length
* 18594 19100: contig of 507 bp in length
* 19101 19854: contig of 754 bp in length
* 19855 20864: contig of 1010 bp in length
* 20865 21609: contig of 745 bp in length
* 21610 22836: contig of 1227 bp in length
* 22837 23742: contig of 906 bp in length
* 23743 25677: contig of 1935 bp in length
* 25678 26700: contig of 1023 bp in length
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* 32697 33898: contig of 1202 bp in length
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* 37228 38230: contig of 1003 bp in length
* 38231 40102: contig of 1872 bp in length
* 40103 40978: contig of 876 bp in length
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QY 121 tgcctcaagtaattatagattccatgcatcccatcaagaactcaatgacttctca 180
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 ORGANISM Homo sapiens
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 Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 152794)
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
 Baker,J., Baldwin,J., Barna,N., Beckwith,R., Benn,J., Brown,A.,
 Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
 Cooke,P., DeRubeis,K., Depayre,E., Devon,K., Dewar,K.,
 Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C.,
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 Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
 Karatis,A., Lehoczy,J., Lien,C., Locke,K., Macdonald,P.,
 Karagas,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J.,
 Meidrim,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J.,
 Naylor,J., Nijhoff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,
 Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P.,
 Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,
 Tesfaye,S., Toruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,
 Wheeler,J., Wu,X., Wymann,D., Ye,W.J. and Zody,M.
 Direct Submission
 Submitted (01-SEP-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Dec 3, 1999 this sequence version replaced gi:581556.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submission@genome.wi.mit.edu
 ----- Project Information
 Center project name: L2049
 Center clone name: 343_C_10

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 33 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
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ORIGIN
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Db 30295 AATGTTAGACCTTAACCAATTAACCAATTAACCAATTAACCAATTAACCAATTAACCAATTA 30354

QY 629 ataggatggcgaaggaactctatgactgaaacacaaagaacaaatggcaacaaacaa 688
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 30355 ATAGGCATGGGCAAGAGACTTCATGACTAAATACGAAAGTGTGGCAACAAAGCCAAA 30414

QY 689 atgacaacaaagatcccaatlaactaaagagcttctgacagcaaaagaa---atcacc 745
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 30415 ATAGACAAATGAAGATCTAAT---TAAAGAGCTTGTGCACACAAAGAACTACCATC 30469

QY 746 agagtgaacagagatctcaagaatggagaatatttaccatctaccatctgacaa 805
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 30470 AGAGTGAACGCGAATATACAGATAGGAGAAATTTTGGCATCTACCATTTGATTA 30529

QY 806 gggcctaatacgaatctcaacaaagaactaaacaaatttgcaagaacaaataacaa 865
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 30530 GGGTATATCCAGAACTACAAAGAACTTAACCAATTT---ACAAAAAATTAATAACA 30586

QY 866 ccccatcaaaaagtggaagaagatatgaacagacactctcaaaaagagacattatgc 925
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 30587 ACCCTTGAAAAGTGGCAAGGATATGAACGACACTTCTCAAAAAGAACATTTATGC 30646

QY 926 agccaacagacagatgaaaaaatgctcatcatcaactgagccatcaagagacatgaaatcaa 985
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 30647 AGCCAAAAAACACATGAATAAAAAATGCTCATCATCATCTGCATAGAGAAATGATATCAA 30706

QY 986 aaccacaatgagatcacatctcacaccagttagaatggaatcaataaaagtcaagaa 1045
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 30707 AACCAAAATGAGATACCATCTCACACAGATGGAATGGCATCATTAACAAAGTCAAGAAA 30766

QY 1046 caacagtgctggaagagtggtggaagaatagaacacttttaactgtgtggagcgtg 1105
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 30767 CAACAGGTGCTGGAGGTGAGTGGAGAAATAGGAACGCTTTTACACCGTGTGGGGAGTG 30826

QY 1106 taacactagttcaacacattgtgaaagacagtgtgacgattccctcaagaatctagaataga 1165
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 30827 TACACTAGTTCAACCAATTTGTGGAGACAGGTGTGATATCTCAAGGTGTNAAACATA 30886

QY 1166 aatataatttgaccacgcatcccatctactggtatgtaacccaagatataaatcatg 1225
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 30887 AATACCAATTTGACCCAGCAGANTCCATTACTGGCTATATACCCAAAGATTATTAATCAAG 30946

QY 1226 ctgctataaagaacatgtgacatgtaagtattatgtggacatttaacaatgcaagaagc 1285
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 30947 CTACTATTTTCTCTTGGACAGAGTNTGTTATCCGCTTGTGGGTGCGTACGAAAGACT 31006
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OY	1286	ctggacacccaacaaatctccacgctggtgtagacggtatgaagaatctggcagtata	1345
Db	31007	TGGAGCCCAACCAATGTCACCAATGATGACTGGATTAAAAAATGTGGCAGCTAAA	310666
OY	1346	cacagctggaaatactatgcaccataaaaaaggaatgaattcagctcctcttgaaggacatg	1405
Db	31067	CACCATGGAATACATGACAGCCATAAAAATGATGATTAAATGCTCTTTAGGACATGG	311267
OY	1406	atgaaagttggaaaccatcatctcttggccaacatcatacaaggttagaagaacccaacccc	1465
Db	31127	ATGAAGGCTGGAACCATGATCTTGTGGACCAACTATACAAAGGACAGAAAAACAAGTACTGA	311868
OY	1466	atgtcttcacatcatgctgggaattggaacaattggaacacttagacacaggttggggaac	1525
Db	31187	ATGTTCTCATTCATATAGTGGGGAACAGCAATGAGAAACCTTGAGCACTGGTGGGGAAC	312466
OY	1526	atcacacaccaaagggcgtcgtcggtggcctgggggaaggggagagatagcatagaagata	1585
Db	31247	ATCACACACTGGGGCGCTCTCATAGGGGTGGTGGCAAGGGGAAGGAGTACGATTAGGAGAAA	313066
OY	1586	taccctaatgtaaaataagtaagttaaggggtggcgacataccaatattggaattatataata	1645
Db	31307	TACCTTAATGTAATACACAGATTAAAGGGGTGCGACACACCAACATATGGACATG- TAAAT	313644
OY	1646	acgtacaacaacctgcacattgtgcacatgtacaccttagaacttaaaaagataataaaata	1705
Db	31365	ATGTACAAACACTGCAGCTGTGACACATGTACCCTAGAACTTAAAGTATATATAAAAAAA	314244
OY	1706	aataaataataataaaataaagaattaaaaaactcaatcaatgaaactaatctttatc	1765
Db	31425	GAATAAGAAAAAAMAAATCTATCTACACACTCTTTCTTTATAGCTTCATCTTTC	314844
OY	1766	tgaataaataatctcaaaaaaaaacacactgatagtctccacactgtccagcttttgt	1825
Db	31485	TAAAAAGTACTCAGCAAAATGATGAAGATATTCTATCTCCACATTTACAAAGCTTTGTA	315444
OY	1826	ttagtgcgcgtgtctgttgggttatctactcaagaataccttggccacactcaatgtcctg	1885
Db	31545	AAGAAATTCCTCTTTTGGG-----CTGGGACAGGTGGCTACAGCTTG	315888
OY	1886	agagatctcccacaaatttctctgtgtgttccatgattgtatgtctcctaagttcaattt	1945
Db	31589	TAAATCCACCCACGACATT-----GGAGGGGCTAGGGGGGAGACATCCGTAGGTCAG	316424
OY	1946	gaactgattcttgatataagacaagatagaagcttaagtctcatctcatctgatatgatt	2005
Db	31643	GAGTTCAGAGACACCCCTGGCCAGGCGCAGGGCGGTGGCTACGCCCTGATATCCAGAGA	317024
OY	2006	atccagcttctccagacaattatctgaaggattgtcttctcccttatatctgtgctc	2065
Db	31703	CTTTGGGAGGCCAA- GCAGGCGAGTATCAGAGGTAGAGATCGAGACCATCTGGCTAA	317614
OY	2066	ttttgtcaaaaattgttccactgtatgaatgaagattcaattctctgttctctatctgt	2125
Db	31762	CACGGTGAACCCCTATCTCTACTACTAAAAATACAAAAAATTACCGGGCGTGGCGGGC	318214
OY	2126	tccactgtctatgtgtctgttttcaatgcagctactatgtctatttgggttgtctaatgct	2185
Db	31822	GCCCTGTACTCCAGCTACTCGAGAGCTGAGGACAGAGAGGTTCTTT-----TT	318668
OY	2186	tgtataatttgaagctagataataatgattccctcctgatttactcttctgtctt--caga	2243
Db	31869	TCTTTTCATATGAATTTAGAACAGTATTTTACTGCTCTGTGTAATAAGCAATTTGGTACT	319288
OY	2244	tagcttggctactcttgggtccttgggtgttccatgtaaatcttgaattttttcttct	2303
Db	31929	TGGATAGCAATAAACATTGAATCTGTAGATCACTTTGGGCAATTTATATGATTTTTCGA	319888
OY	2304	attcttggaaagaatgtaattgtatatttggtagtatgcatctgaatctgtgaattgct	2363
Db	31989	ATTATATGAGCATGGAATGTTTTCATTTG-----TGTCAACATGATTTCT	320355
OY	2364	ttgggtatgataaactcttccaatctataagaatgtaatactcttcaatttttttttg	2423

Db	Accession	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	33058	GACATGAGGAAATTTACATGTTTCATGTCGCCGCTTGATTTGGTTGCTAGTAATTTGGTTGA	33117														
Qy	3492	ggatttttaacatcaatatcatccacagagaataacgacctgagcttgcattcttttttgatgac	3551														
Db	33118	GGATTTTGTGTCTATGTTTCATGTCACAGAGAAATTTGGGCTGTAGTTTCTTTTTCATTTTAT	33177														
Qy	3552	tttgtctgcttttggtatccagggaataactgacctgacctgagatagatttggaaatc	3611														
Db	33178	GTTTACTAAATTTTGTAGTATCATGATTTATTTCTCCATTTGTAAGATAGTATAGAGAGATC	33237														
Qy	3612	cctccctctctatctgtttccaggagttgagtaacggttgatc---agttctcaagc	3668														
Db	33238	TGTCCTCCACAGATTTTGTATTAATAAGTGCACAGAGATTTGGTACTGGCTGTTCTTTGTATG	33297														
Qy	3669	tttggtagaattccagcagtgaaactctggctggccacagactcgtt-----	3714														
Db	33298	TCTGGTAGATTTTGGCTGTGAAATACGCTCTGTTGCAGAGATCTTTTGGTTAGATGTTTC	33357														
Qy	3714	-----actgttattatctctgttccaggttttagatttcttcag	3752														
Db	33358	TATTAATGATTCATATTTAGAACTATTTCTATTTGTTGTCAGAGGTTTGAATTTCTCTTGC	33417														
Qy	3753	gtccaatatgttgtagagatgtagtctataggagtttatacatcttctcagatttccaa	3812														
Db	33418	ATTCAATCCAGAGAGGTTGTATGTTCCAGGAAATTTATTCATTTCTCAGATTTTATTC	33477														
Qy	3813	ttttatgcatataattgtctcagtagtagccacaaatgacaccttgaaattcgtatc	3872														
Db	33478	TTTTTGTATTATGAGAGTATTTTATATAGCCTTAAGAGATCTTTGATTTCTGTGGATC	33537														
Qy	3873	agtgtaatgtctcctctcttcatcttcctgatttattattatttggtcttctctcgt	3932														
Db	33538	ACTTATTAATGTTTCTCTTTGTCTATTTCTGATCGTACTATTGTACCTCTCTCTTTT	33597														
Qy	3933	ct 3934															
Db	33598	TT 33599															
RESULT	6	AC007282/C															
LOCUS	AC007282	192151 bp	DNA	HTG	05-JUN-1999												
DEFINITION	Homo sapiens clone NH0484N09, *** SEQUENCING IN PROGRESS ***	4															
ACCESSION	AC007282																
VERSION	AC007282.2	GI:5001487															
KEYWORDS	HTG; HTGS_PHASE1.																
SOURCE	human.																
ORGANISM	Homo sapiens																
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;																
AUTHORS	Eutheria; Primates; Catarrhini; Homiidae; Homo.																
TITLE	1 (bases 1 to 192151)																
JOURNAL	Waterston, R.H.																
REFERENCE	The sequence of Homo sapiens clone																
AUTHORS	unpublished																
TITLE	2 (bases 1 to 192151)																
JOURNAL	Waterston, R.H.																
REFERENCE	Direct Submission																
AUTHORS	Submitted (09-Apr-1999) Genome Sequencing Center, Washington																
TITLE	University School of Medicine,																

[illegible]

QY	835	taaaacaaatttgtaagaagaaaaaatcaaaacaccacccaataaaaagtgtggcgaagaagtatga	894
Db	59398	CAAAACAATTTACAAAGAAAAA-----AAACCAACCCCATPAAAAAGGGGCAAGACATGTA	95344
QY	895	acagacactctcaaaagaagacattatgacgcccacagacaagtgaataaaatggtcat	954
Db	59343	ACGACACTTCTTAAAGAGACATTTATGCGCCAAAAAACCTTGAAAAATGCTCTC	95288
QY	955	catcaactgpcatcagagacatgycaaatcaaaacacaatgagatatacatctcacccag	1014
Db	59283	CATCACTGGCCATCAGAGAAATGCAATCAAAAACCAATGAGATACATCTCACACAG	95222
QY	1015	ttagaatgycatcatctaaagaagtcaggaacacacaggtctgtgagagatgcygagaaa	1074
Db	59223	TTTGAATGGCAATCATTTAAAAAGTCAGGAAACMACAAGTGGTGAGAGATGTGGAGAAA	95166
QY	1075	taagaacacttttaacacttttggtggagactgtaaacctagctcaacactitgrygaagacag	1134
Db	59163	TAGAACACTTTTACACTCTGTGTGGAGCTGTAACCTTGTTCAACCATTTGGAGATGACAG	95100
QY	1135	tgtgycgactctcacaaggaactagaactagaatactcatggaaccagccatcccat	1194
Db	59103	TGTGGCCATTCCTCAGAGATCTGAACTGTAATACCATTTGACCAACCATCCCATTTAC	95044
QY	1195	tgggtatgtatcccaaaaggattataatcatctgctgctataagaacacatgycacatgtat	1254
Db	59043	TGGGTATATCCCAAGGACTATTAATCTAGTGTGTATTAAGACACATGCAACATATGT	95986
QY	1255	ttattgtgacacttcacaatagcagaagaccttggacccaaccacaatgctcatcagtg	1314
Db	59893	TTATGTGGCATTTATTCACATATGCAAAAGACTTGGACCAACCAATGTGGAACATGA	95922
QY	1315	tagactggaactaaagaaatgtgycatgtatatacagatggaatattatgacccat-aaaa	1373
Db	58923	TAGACTGTGATTAAGAAAAAGTGGCACTATACCCATGGAATACTATGCAACCATAAAA	95866
QY	1374	aggaatgagttcaagtcctcttttagagagacatgaatgagttgaacccaatctcttgca	1433
Db	58863	ATGTGTGTTCACTGCTCTTTGTAGGGACATGTGATTAATGTGAATCTCATTTCTCGTA	95800
QY	1434	aactatcacagaagatagaagaaacccaacacacacatgtcttcacatagatggygaattgaa	1493
Db	58803	AACATGCGACAGAACAAAAACCAACGCCACATTTCTGCATCATGATGATGGAAATGAA	95744
QY	1494	caatgagacaacttagacacaggtgtggygaacatacacaccagggcctgtcgttggcgt	1553
Db	58743	CAATGTGAAACATGTGACACAGGAAGGGGAACATCACACTCTGGGGACTGTTGGGGGTG	95864
QY	1554	ggggggaaggggggggaatgtgcatcttggagatattacttaatgtaaagaatgattaaagg	1613
Db	58683	GGGGGAGGAGGGGAGTATGCAATGTGGGAATATPACTATATCTGTAGGAGATGATTTATGG	95622
QY	1614	tgcagcatcacacaatggygacatgtatatacagtaacaacactgycacatitgycacat	1673
Db	58623	TGCGATGTGCACACATAGGCACATGTATACAT-ATTTAATCTAAGCTGCACATGTGCGCAT	95856
QY	1674	gtacccctagacttaaaagtataataaaaaataaataaaataaataaaaaa-----	1729
Db	58564	GTAACCCCAAAACTT-AAAGTAT	95800
QY	1729	-----	1729
Db	58505	AGTATCCGTTTATGTCTTGTCTGCTTTTAAATGGGGTGTGTTGTTTCTTGTA	95444
QY	1729	-gattaaaaaacatcatcaatgaacataattttctcgtatataaataatctcaaaaa	1786
Db	58445	TTTGTTTAACTTCATATATGATGCTGGATATTAGACTTTGTTAGATGCAATAGTTTGCA	95388
QY	1787	aaaaaacac-----	1796
Db	58385	AAATTTTCCCCCATCTTTAGGTTGTCTGTCTTACTGCTGTGATTATTTTGGTGTGCAGAA	95322
QY	1796	-----tgaatgtatcccatctgcatcttgcgttgcgtgtgctgtgtgtg	1845

D	58325	GCTCTTAAGTTAATTAGATCCCACTTTGTCAATTTTGGCTTTGTGTGAGATTCGTTTGG	58266
Q	1846	ggtaattacaaagaacattcttgcccactccaabgctcttgagagctccccaagtcttc	1905
D	58265	TGTCATCATGATGAATCTTTGTGCCGCTATGTCCTGAATGATGATGGTTGATGGTTGTC	58206
Q	1906	cttgaagtagcttcaatcggtttgagctc-----aaagtcatttgac	1948
D	58205	TTCCCGGCTTTTATATTAATTAAGTTTGGCTTTACATTTAAATATTTAAATCAATCTTTGAG	58146
Q	1949	ttgatttttgatataagagaagtagagctagaatttcaatttcaatctgataagatatac	2008
D	58145	TGAATTTTGTATATAGGTATAGGTATAGGTATCCAGTTTCATCTTCTGCATATGCTCCG	58086
Q	2009	caatttcccaagaacaatttatbaagagaatgctcttcc-----ttatatcttgct	2064
D	58085	CAGTATCCCAAGCAACATTTATTTGAAGAAGAAATCCCTTCCATTTGGTTGTTTGTGA	58026
Q	2065	cttttgcataaattagctcaacgtatagatgatatctctgcttctctatctcg	2124
D	58025	GGTTGTCTAAAGATCAGATAGTTGTAGCTGTGAGCTTATTTCTGGGTCTCTGTCTGTCG	57966
Q	2125	ttccaagctatagtctgcgttttcaagcgaactacatactatcttgaggtgc-tatagc	2183
D	57965	TTCCCTTGGCTATATGTCTGCTTTTGTACCACTACATCTCTTTGGTTACGTAGCC	57906
Q	2184	tgtagtaaatitgaagtcagataataatgattccctcgtatattatcttttgctcaga	2243
D	57905	TGTAGTATAGTTGAAGTGGGTAGTGTGATGAGCTAGCTTGTATTTTCTTAGGA	57846
Q	2244	taagcttggcctacccctggtctctttgctggttccatgataatttagaatctttctct	2303
D	57845	TTGCTTTGGTATTTGGCTCTTTTGTGCTATATGAATTTTA-AAAGATGTTTCTCT	57787
Q	2304	attctcggaagaatgcattcgatattcttgagtaattcattgataatcgtatagctct	2363
D	57786	AGTCTTTGAAGATCTCATGGGGTTTATAAGATACATGATGATCATTAATTTAT	57722
Q	2364	ttggtagtagaac-----attctccaactataagcaatgaaatc	2407
D	57726	TTGGCGAGTATAGCCCATTTTAATGATATGATCTTTCTATCCAGAGCATGAAATGTT	57667
Q	2408	ttcatcttttttttggtgcctctcaactctcttggtgaacaatttaagtcttaacg	2467
D	57666	CTACCAATTTG--TTGTGTATCCCTGACCTCTTTGAGCGAGTGTATGTTCTCTTG	57610
Q	2468	tagaagatcttcaactctcttggtta-----attactagagacttattatcttagct	2522
D	57609	TAGAGATCTTCACTCTCTAGTTAGCTGATCTCTTAGATTTATCTTTTATAGCA	57550
Q	2523	atgttcaacaggaattctcttgatctcttttcagagatgtctccctgtatgacataaga	2582
D	57549	GTTGGAATGAGGAGTTCATTCCTGATTCAGTCTTGTGGCTTGT---TGTGTGGTATAG	57494
Q	2583	aatgctgatttttggtccgggtgcggtggtgcacgctgtaaccagaacatttggtgag	2642
D	57493	AATGCT-----AGGATTTTGGACATATGATTTTGTATCCTAGACT	57452
Q	2643	ccggagcggtgcgaatcagagatcgagaagatcagaccatctggtatacaacggtgaac	2702
D	57451	TTGCTGAAGTTGTTATACAGTTTAGAAGCTTTTGGGGTGAGACTATGGGGTTTGTATA	57392
Q	2703	ctgctctctataaaaaacacaaaatttagcgggtgcgttggtgacggtcgttggtcc	2762
D	57391	TGTAGATATATGTCATCTGCACAAACGATTAATTGACTCTCTGTTCTATATGGGATACC	57332
Q	2763	agctactacaggaagctgagacaggaagaatagagtgaaaccgggaagcggtgacgtgc	2822
D	57331	TTTATTTTCTTTTACT-----TGCTGATTTGCTCTGCG	57299
Q	2823	agccgagacggcaactgcatcgccgtggcggaagaagggagatctcgtctcaaaa	2882

D5	57298	CAGGATTTCCATNGCATTTGACTTACAGAGTGGTAGAAGGCGATCCCTGCTTTGGC	572393
OY	2883	aaaaaanaaagaanaaagaanaaagaaycctgaattttgtaagaatltgtatac	2942
D5	57238	ACGTTTTTAAGC---GGAATFAGGCAATTTGGTTTGATTTACATCCATTTGTTTGAAGCA	57183
OY	2943	tgtgacctgttggaatttgtgatacgttctaagtgttttgggtgaagctttagtt	3002
D5	57182	CATGACGCTGAATTAAGTTG-----AGGTT	57155
OY	3003	ttccaataataaagaatcatcctgaaacaagataatttgacttcttccttccaatt	3062
D5	57158	TCTTTAAAAAANAAGAGTGAGGACCATTTGCCATT-----	57113
OY	3063	gtagccacttcttcttctctctgtctgattacaagactccagatattgttgaa	3122
D5	57119	-----	57113
OY	3123	aaccagtgtgaagtgggacacctgtgtctctagatccttgagaagggctttagttct	3182
D5	57119	--CAGTGATGATGTGGCTGTGGATTCACTAGGATTAAGA-----	57073
OY	3183	ccctatcatcttgacacagcgtgcgcgtcatctcaatgagcttcttcaitgaagt	3242
D5	57077	--CATACCTCGAATTAATA-----ATATCTTTCTTATATTCTAGGT	57033
OY	3243	atgttcctctctatacaagcttttttggaaattttatcatagaaggatgtgaatttat	3302
D5	57035	ATGGTCCTCTCATACCTAGTTATTAGAGAGTGTTGACATGAATGATTAATTAATTAAT	56974
OY	3303	caa-----ctgcttctttagatcatacctcgaaatgaataatggttttgcctcatctgt	3359
D5	56975	CATAGCTGCATTAATCTGCATCTATTGAATATATCATATGAGGTTTGCTTTAAGTCTGT	56910
OY	3360	agataagacatatcacacagtgttgattgatactgatactgacaacacctgcattcccgga	3419
D5	56915	TATATGGATGATGCATCATTTATTGATTTGTATACGTCAACACCACTTGATGCCAAGCA	56855
OY	3420	taaatccacctgtgatacgaatgagatcctttaaataatgttgtaaccacagttgcta	3479
D5	56855	TAAAGCCTACTTGCACAGTGGTGGGCAAGCTTTTGATCTGCTGAATTAAGTTGCGCA	56796
OY	3480	gtaatttgcctggagatttttaatacaatttcaacgaatactggccgttagcttctt	3539
D5	56795	GTAATTTGTTGAGGATTTTGCAATCATATGTCAACAGATATGGCTTAAGTTTCTT	56733
OY	3540	tttttgatgtaactttgtctgtgtttgtgatacaggttaactgagcttgaagaatgaat	3599
D5	56735	TTTTGTGTAATGTCTGCCAAGTTTT---CATCAGGCTGATGCTGGCCTCATGAATGAGAT	56675
OY	3600	tttgaagaatctccctccctctctctatgcttcagagtagtttgagtaagcttgbatag--	3658
D5	56678	TGGGGAGGGGCTCCCTCTCTCTCAATTTTGGGGAATGATTGATAGTAAGTAGTACAGCT	56619
OY	3658	-ttcttcaagcttcttgtagaatttcagcagtgaaatccttcgggtccag-----	3706
D5	56618	CTTCTTGTGTAACCTGGTAGAATTCAGCATAGATCAATCATCTGGCTTGGGCTTTTCTGG	56555
OY	3706	-----atctgttactgttatttcactctgttcaagttt	3739
D5	56558	TTGGTAGGCTATTATTATTATGCTTCATTTTCAGAGCTGTATTATGCTCATTTACAGGAGATT	56499
OY	3740	agatttcttcaaggtcccaatatctgtagagatgtagtattgtataggaatttataacttctt	3799
D5	56498	CAGTTTCTCTCGTTCAGTCTTTGGGAGGGATATATGTGACATAGAATTAATCATATTCTT	56433
OY	3800	ctagatttcccaatttatctggcatataatctgctcatagttagccacaatgatacctttga	3859
D5	56438	GGAGATTTTCTAGTTTATTATTCATAGTGGTGTCAATAAATTCCTAATGATGTTGTTGTA	56379
OY	3860	ttctgatatlacaggttgaatgctccctcttcaattcttgattattattattgtgtc	3918
D5	56378	TTTTTGTGGGGCTCAGTGGCAATATCCCTTGCTGTGTGTGGTGTCTTATTTTGAATC	56320

LOCUS	AC006288	220218 bp	DNA	PRI	16-JAN-1999
DEFINITION	Homo sapiens chromosome 9, clone hRPK.295_D_22, complete sequence.				
ACCESSION	AC006288				
VERSION	AC006288.1	GI:4160142			
KEYWORDS	HTG.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1 (bases 1 to 220218)				
TITLE	Birren,B., Linton,L., Nusbaum,C. and Lander,E.				
JOURNAL	Homo sapiens chromosome 9, clone hRPK.295_D_22				
AUTHORS	Unpublished				
REFERENCE	2 (bases 1 to 220218)				
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baker,J., Baldwin,J., Barna,N., Beckert,R., Benn,J., Brown,A., Castle,A., Cerny,J., Colangelo,M., Collins,S., Collumore,A., Cooke,P., Dearlano,K., Depayre,E., Devon,K., Dewar,K., Donelan,L., Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Hecena,L., Horton,L., Howland,J.C., Jones,C., Kann,L., Karatas,A., Lechoczky,J., McDaniel,P., Marquis,N., McEwan,P., McCurt,A., McKernan,K., Meldrim,J., Molla,M., Morris,W., Morrow,J., Mychalecky,J., Naylor,J., Niliot,F., O'Connor,T., O'Donnell,P., Pavlin,B., Peterson,K., Pollard,V., Riley,R., Roberts,D., Roy,A., Severy,P., Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A., Testaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (05-JAN-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA				
REFERENCE	3 (bases 1 to 220218)				
AUTHORS	Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baker,J., Baldwin,J., Barna,N., Beckert,R., Benn,J., Brown,A., Castle,A., Cerny,J., Colangelo,M., Collins,S., Collumore,A., Cooke,P., Dearlano,K., Depayre,E., Devon,K., Dewar,K., Donelan,L., Doyle,M., Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L., Karatas,A., Lechoczky,J., Liu,C., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurt,A., McKernan,K., McLaughlin,J., Meldrim,J., Molla,M., Morris,W., Morrow,J., Mychalecky,J., Naylor,J., Niliot,F., O'Connor,T., O'Donnell,P., Pavlin,B., Peterson,K., Pollard,V., Riley,R., Roberts,D., Roy,A., Severy,P., Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A., Testaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-JAN-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA				
COMMENT	On Jan 16, 1999 this sequence version replaced gi:4156127. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html .				
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Matches 2116; Conservative 0; Mismatches 402;

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RESULT 8
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LOCUS AC002564 94320 bp DNA PRI 26-SEP-1997
DEFINITION Human BAC clone RG164L14 from 7q21-q22, complete sequence.
ACCESSION AC002564
VERSION AC002564.1 GI:2439514
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 94320)
AUTHORS Murray,J., Wohlmann,P and Antoniou,B.
TITLE The sequence of H. sapiens BAC clone RG164L14
JOURNAL Unpublished (1997)
REFERENCE 2 (bases 1 to 94320)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-1997) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT SUBMITTED BY:

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GRB/CH7> or send ..

mailto:egreen@nhgri.nih.gov

SOURCE INFORMATION:

This clone is from the first release of the human BAC library. The library contains cloned DNA from a human male fibroblast cell line 978SK. See: Shitaya et al., *Proc. Natl. Acad. Sci. USA* 89:8794-7 (1992). Kim et al., *Genomics* 34:213-8 (1996). The clone is available from Research Genetics, Inc. (<http://www.resgen.com>).
VECTOR: pGloBAC11
selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is Rg11p10, 200 bp overlap; the clone sequenced to the right is R6005F13, 200 bp overlap. Actual start of this clone is at base position 35127 of Rg11p10; actual end is at 16949 of R6005F13.

This clone contains STS SWS2344 (NID:q1254768)

source

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidi; Homo.
1 (bases 1 to 73029)
REFERENCE
Lloyd,D.
AUTHORS
Direct Submission
JOURNAL
Submitted (17-NOV-1999) Wellcome Trust Genome Campus, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humgen@anger.ac.uk Clone requests: clonerequest@anger.ac.uk
on Nov 18, 1999 this sequence version replaced gi:6053948.
COMMENT
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n s separate
segments.

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AUTHORS	Stone,N.E., Keseler,I.M., Schmutz,J.J., Shang,J., Cox,D.R. and Myers,R.M.		
TITLE	Direct Submission		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 161326)		
AUTHORS	Stone,N.E., Schmutz,J.J., Cox,D.R. and Myers,R.M.		
JOURNAL	Direct Submission		
TITLE	Submitted (28-JAN-1998) Department of Genetics, Stanford Human Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA		
REFERENCE	3 (bases 1 to 161326)		
AUTHORS	Stone,N.E., Keseler,I.M., Schmutz,J.J., Shang,J., Cox,D.R. and Myers,R.M.		
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JOURNAL	Submitted (08-NOV-1998) Department of Genetics, Stanford Human Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA		
COMMENT	On Nov 9, 1998 this sequence version replaced gi:3694642. Quality: Phrap Quality >=40 99.8% of Sequence; Estimated Total Number of Errors is 0.8		
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 Db 9488 AGTGGCGGATTCCTCAAGGATCTAGAACTAGAAATACCATTTGACCCAGCATCCCAT 9547
 QY 1193 actggtatgtacccaagagatataatcatgctgctataagacagacatgacatgtat 1252
 Db 9548 GCTGGGTATATACCAAGGATTAATATCATGCTGTATAAGACACATGACACA--CAT 9605
 QY 1253 gttatttgcagactatcacatagcaaaagcctggaacccaacaaatgtccatcaat 1312
 Db 9606 GTTATTGAGGCACTTACCATATAGCAAGACTTGGAAACCAACCAATGTCATCAT 9665
 QY 1313 ggtagacgtgagtaaaatggtgcatacacaagtgtgaatattatgacccat-aa 1371
 Db 9666 GATAGACCGGATTAAGAAATGTGGACATATACACATGAAATACTATAGCCCATATA 9725
 QY 1372 aagaatgagttcagctcttgtgagacatgagtaaggttggaaacacatcttctgag 1431
 Db 9726 AAAGATAGATTTCATGCTCTTTGTAGGACATGATGAAAGTGGAAACCATATCTCAG 9785
 QY 1432 caaactlacaagaatagaaacaaacacacacatgtctcactcatatggtggaaatg 1491
 Db 9786 CAACATATGACAGACAAAAAACCAACACCGCATGTTCTCATGATGAGGGGATAG 9845
 QY 1492 aacaatgagacacttaacacaggtgtggagacatcaacacccagggcctgtctggagc 1551
 Db 9846 AACATGAGAACACATGACACAGGAGGGAACATCACACCTGGGGCTTTGTGGGG 9905
 QY 1552 tggggggaagggggaagatagcatagagagatataccataatgaagaatgactaatg 1611
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 QY 1612 ggtcagacataccaacatgagacatgltatatacgtatacaaacactgacatgtgcac 1671
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 QY 1672 atgtacctagaacttaaaagtataataaataaataaataaataaataaagat 1731
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 QY 1732 taanaaacatcaatgaataaactaattttatctgataaataatctcaaaaaa 1791
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 QY 2020 gacaattatgaaggagatgtcttcccttataatc---ttggccttltgtcaaaa 2076
 Db 10329 GACATTTATTAATAAGGGAATCTTCCCTATTTCTTTTCTTTGACAGTTTGTCAAG 10388
 QY 2077 attagttacgttagatgtatgattatcttcttcttcttcttcttcttcttcttct 2136
 Db 10389 ATCAGATGCTTTTGTATGTG-----TTACTTGTAGGACTTTGTTCTGTCCATGGGCTT 10443
 QY 2137 atgtgtcttcttcatcagactacatgactatgttgtgtgtatagc--tgtgtataat 2194
 Db 10444 ATGTATCTGTTTGTGACAGATGATGCTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTT 10503
 QY 2195 ttgaagtcagataatagatcttctctgtatcttcttcttcttcttcttcttcttctt 2254
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RESULT 11
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 LOCUS AC004068 110401 bp DNA PRI 10-APR-1998
 DEFINITION Homo sapiens chromosome 4 clone B380B14 map 4q25, complete
 sequence.
 ACCESSION AC004068
 VERSION AC004068.1 GI:3046280
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 110401)
 Stone, N.E., Keseler, I.M., Schmutz, J.J., Shang, J., Cox, D.R. and
 Myers, R.M.
 TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 110401)
 Stone, N.E., Schmutz, J.J., Cox, D.R. and Myers, R.M.
 TITLE Direct Submission
 JOURNAL Submitted (28-JAN-1998) Department of Genetics, Stanford Human

QY	241	agataactctaaagcaaaagcaaaagctggaagcactatgctactgacttccaactt	300
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QY	660	caccaaagcaatggaacaaaaaaccaaatgacaacacagatccaatctaaactaa	719
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QY	837	aacaaattgcaagaaaaaatcaacaaccccatcaaaagtggtgcaagagatagac	896
Db	77113	AACAAATTTACAGAAAAAAA-CAACACACCCCATCGAAGAGTGGGTGAAGATATGAAC	77171
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QY	1077	ggaacacttcaacatggttgggtggaactgtaactatgctcaacacttgggaagacagt	1136
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QY	1137	tggcgattcccaaggatctagaactagaatatcatcttgaccacgcatcccatctagt	1196
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QY	1197	ggtatgtacccaaaaggattataatactatgctgctataaagaacatgacatggtatg	1256
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OY 2484 ctttgtaataactaggaacttatttatttttgatctatgttaacggattacttc 2543
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OY 2664 gtcagagatcgagacacatctcgtctaacacaggtgaacctcgtcttataaacaca 2723
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OY 2724 aaaaattgacggcggtgtgtgtgcggcgctgtgtcccaagctcagagagcgtaggc 2783
DB 79029 AAAAAATTACCCGGGGTGGCGGGTGGCTGTAGTCCAGCTACTGGGATGCTGAGGC 79088
OY 2784 aggaataatagatgaacccggagcgagcgagtcagtagagccgagacagcgcaacttga 2843
DB 79089 AGGAGATGTGTGAACCCAGAGGGGAGAACTTGCAATGAGCTATCATGCACTGCA 79148
OY 2844 gtccagcttgagcgagagagagagagctcgtctcaaaaaaaagaaagaaag 2903
DB 79149 CTCAGCTGTGGGTGACAGGACAGACTCATCTCAAGAAAAAAGAAAAAAGAA 79208
OY 2904 aaaaagaatgctgatttt 2922
DB 79209 CCAAGACCAAGTGTATT 79227

RESULT 13
HSDJ149L1/c
LOCUS HSDJ149L1 118205 bp DNA HTG 23-NOV-1999
DEFINITION Homo sapiens chromosome 6 clone RP1-149L1, *** SEQUENCING IN
PROGRESS ***, in unsorted pieces.
ACCESSION AL080275.8 GI:5870455
VERSION AL080275.8
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 118205)
AUTHORS Nickerson, J.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-1999) Wellcome Trust Genome Campus, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humgen@anger.ac.uk
On Sep 12, 1999 this sequence version replaced gi:5823982.
IMPORTNOTE: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known: 800 n's separate
segments. Unfinished: djl149L1 Contig_ID: 00596 acc=AL080275
length: 1095 bp Unfinished: djl149L1 Contig_ID: 02066 acc=AL080275
acc=AL080275 length: 3552 bp
length: 79988 bp Unfinished: djl149L1 Contig_ID: 02287
acc=AL080275 length: 3552 bp
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES
Location/Qualifiers

source 1. 118205
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="RP1-149L1"
/clone_1b="RP1-1"
BASE COUNT 34958 a 22164 c 23550 g 35919 t 1614 others
ORIGIN

Query Match 6.1%; Score 153.2; DB 32; Length 118205;
Best Local Similarity 73.2%; Pred. No. 8.7e-256;
Matches 2164; Conservative 0; Mismatches 753; Indels 39; Gaps 14;

OY 1 aggaaccttcaaggaagaaactcaaacacactgctcaacgaagtaaaagagacacaca 60
DB 116479 AGGACCTCTTAAGAGAGAACTCAACCAACCACTGCTCAATGAATTAAGAGATCAAAACA 116420
OY 61 aatgagaagaacattccatgctcatgtagtaggaataatcatatcaatgaatgagccatc 120
DB 116419 AATGGAAGAATATTCATCTCATGCTGAGGAGAAATCAATATCGTGAATATGGCCATAC 116360
OY 121 tgcctcaagtaattatagattccatgctccatcccaagctaacatgacttcttca 180
DB 116359 TGCCCAAGGTATTATTATATTCATATGCTCCATCCCTCAAGCTACCAATGACTTTCTTCA 116300
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DB 116299 CAGAAATGGAAAAAACTACTTTTAAGTTCATATGAAATCAAAAAAGCCCGCATGCA 116240
OY 241 agataatcctgaagcaaaagaacaaagctggaagcatgcttactgacttcaactat 300
DB 116239 AGTCATCTCTAAGCCAAAAGAAAGCAAGCTGAGGCTCAGCTACTCTCAACTAT 116180
OY 301 actacaagagctacagtaaccaaagaacagcagtggtactggtgtaacaaagcagaaatagacc 360
DB 116179 ACTACAGGCTACCGTAACCAAAACGATGCTACTGTAACCAAAACAGATATGAGAC 116120
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DB 116119 AATGGAACAGAAAGAGCCCTCAGAAATATGCAATATCAACATCTGATCTTGG 116060
OY 421 acaaacctgaagaagaagaatagggaaagagatcccttatttaaatggtgttg 480
DB 116059 ACAAAACCTGACAAAACAAAGCAATGGGGAAGGATCCCTATTATTAATGCTGTGG 116000
OY 481 aaactgctagccatagtagtaagaagctgaagctgactcccttccacattacaca 540
DB 115999 AAAACAGGCTAGCCATATGTAGAAAGCTGAAGCTGATCCCTTACACCTATTCA 115940
OY 541 aaatcaatccaagaatgattaaagacttaaatgttagacctaaacataaacccttg 600
DB 115939 AATTTATTCAGATGAGATTAAAGATTAATGTTAGACCTTAACCAATTAACCCCTAC 115880
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DB 115879 AGGAAACCTAGGCAATACCATTCAGGACATAGGCTGGGCAAGGACTTCAATGTCTAAA 115820
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DB 115699 AATTTCTCAATCTACTATCTGACAAAGGCTAATATCCGAATCTCAATGAATCA 115640
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QY	2154	ccagtaactatgctatttgggtgtctctatagctgtgtataatttgaagtcagataatgta	2213
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QY	2214	ttcccccagatttatcttttcttgcttcagaatgttggctactcgggtcgttttgggt	2273
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QY	2274	tccacgtaaattttagaatttttttttctattctctgtgaagaatgctatgtattttg	2333
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QY	2334	ttaagttatgcatgtaactgtctagattgtcgtttggtatgataacatcttccaactcat	2393
Db	114161	----GTGAGACACTACATTTAGTACATTCACAAAAGAAATATGCTGTTAAGTGACAT	114106
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QY	2454	tatagtttccagtagagatcttcaactcttctgttataactagtaacttatttta	2513
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QY	2514	tttttagcatgtttaacaggaattacttcttgaattcttcttccaatgttccctgtta	2573
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Db	113807	CATGCTGAAGAACCCGCTCTCTACTGAAATACAAAAAAATTTACCCAGATGTGCTGGCGGG	113748
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QY	2810	ggaaggtgcaatgtagccgagacagcgcaactcgcagctcagcccgggcggaagaaggagac	2869
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QY	2870	tccgtctcaaaaaaanaaaagaagaagaagaagaagaatgctgtattttgtatga	2929
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RESULT	14		
LOCUS	HS93L7	206784 bp	DNA
DEFINITION	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21.		PRI 23-NOV-1999

ACCESSION AL022401.1 GI:3059060
VERSION HTG; CHM; Choroideraemia; geranylgeranyltransferase component A 1;
KEYWORDS RAB Escort; REP-1; REP1; Tapetochoroidal Dystrophy; TCD.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutharia; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 206784)
AUTHORS Grattham,D.
JOURNAL Direct Submission
Submitted (26-MAR-1998) Chromosome X Project Group
(http://www.sanger.ac.uk/HGP/ChrX/) Sanger Centre, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquires:
humqueres@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
IMPORTANT: This sequence is the entire insert of clone 93L7. During
sequence assembly data is compared from overlapping clones. Where
differences are found these are annotated as variations together
with a note of the overlapping clone name. Note that the variations
annotated may not be found in the sequence submission corresponding
to the overlapping clone as we submit sequences with only a small
overlap as described above.
This sequence was generated from part of bacterial clone contigs of
human chromosome X, constructed by the Sanger Centre chromosome X
mapping group. Further information can be found at
http://www.sanger.ac.uk/HGP/ChrX/
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The true left end of clone 93L7 is at 1 in this sequence. The true
right end of clone dA43C13 is at 36921.
The true right end of clone 93L7 is at 206784.
93L7 is from the library RPCII constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong.
For further details see http://bacpac.med.buffalo.edu/.

FEATURES
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379. .658
repeat_region
/note="AluX repeat: matches 302. .14 of consensus"
683. .984
repeat_region
/note="AluX repeat: matches 302. .1 of consensus"
986. .1168
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/note="5' part of gene beyond this clone; match: CDNAS
X78121 M83773 X57637 U3722 X6728"
/product="dJ93L7.1 (RAB Escort protein 1 (REP-1, RAB
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Choroideraemia protein, Tapetochoroidal Dystrophy (TCD)
protein)"
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Insert size: 144159; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; agarose-1p
Quality coverage: 3.3 in Q20 bases; sum-of-contigs

* NOTE: This is a working draft sequence. It currently
* consists of 38 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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Rhodes

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 TITLE Direct Submission
 JOURNAL Submitted (06-JAN-1999) E-mail contact: humquery@sanger.ac.uk
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 Further information can be found at
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Db	121	GTACACTCCAAAGTCAATTTAAAGAAATCTCTGTGATCCAGCTGGATAGATGACTTTC	100.0%	2567	2567
Qy	121	gtcacctccaaagtcaatttaaagaatactctgtcagctgataagatcgtgacttc	100.0%	2567	2567
Db	181	CCACCAATGCTGCTGAGATGCTGTGCATCATTTGGCTGACTTCAACACTGAGTTGT	100.0%	2567	2567
Qy	181	ccaccaatgctgctgagatgctgtgcacatctgtcgtcagcttccacacagagtgtgt	100.0%	2567	2567
Db	241	GTTCGAGATTCTCCCTGTTGGAATATGAAGATGATTAAGACCTGGCAACCTAGT	100.0%	2567	2567
Qy	241	gttcgagattctccctgttggatatagaagatgatgatacaagaccctgcaacctagt	100.0%	2567	2567
Db	301	GGATGCTAAACATTTTATTTATGTTCCGGAATGGCAAGAGCTTCAAAAGCCCTGAACA	100.0%	2567	2567
Qy	301	ggatgctaaacatlttattatgttccggaatggcaagagcttcaaaagccctgaaca	100.0%	2567	2567
Db	361	GAATGATCCCTCATTTGAGGTGCACTATGTTCTGTGTGGAAGCCCAAGAGGAT	100.0%	2567	2567
Qy	361	gaatgatccctcatlttgaggtgcactatgttcttcttccgaagccagtgaaaggtat	100.0%	2567	2567

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D	1501	CAACCTCCCTTGAAGCGGAGCATGTAAATCGTGGGATACGTGGCGAGACACTG	1560
Q	1501	caacctccctctgaaagcgagggcattgtaaatctggaatcgtgcgtgagacacgtgc	1560
D	1561	CTTCAACAAGCTCATTAATGGACACCGTGATTTGGCCATTGAGTTAGCTCCGAGCC	1620
Q	1561	cttcaaaagctcataetaggagaccctggatcttgcgcatgtgaggtcccgccct	1620
D	1621	TCGATGTGGGCATGCTGCCAGATCCCAAGTCCACATATACGTCCCTGTGACATT	1680
Q	1621	tcaatgtggcactgtctccaagatcccaacgcaattacagtcctctctgagagctta	1680
D	1681	CAGATGTCCTCTTGAACAGACAGATACCCGCAATTGATCAGGTGCTGGGGCGCTG	1740
Q	1681	cagatgtctctctctgacagcagatcccgcaattgatacagtgctgtggcggtctg	1740
D	1741	GGACCTTTCTCTAACACAGGAACACATCTCACAAGGCAATTTTCTATTGTGCTG	1800
Q	1741	ggaccttctctgaacacaggaacacatcttcagcaaggcatcttctatctgtctgct	1800
D	1801	GGACATCCCTGTTATTCTGCTTTGTTTATTAACAATTGGAAGAACTTTGGAAATC	1860
Q	1801	ggacatcctgcttattctctgtgtttgttatagaaactttgaagaaatgtttgaaatc	1860
D	1861	ACACCAATACGAAAAACAAGAAATCCTCAAGTTCCACATGTGACTCTCTCGGACTTA	1920
Q	1861	acaccaatacgaanaaacaagaatctcccaagttcccaagtcctcctctgtgactta	1920
D	1921	TTCTCTTACTACTATCTGGAGAGTGTAAAGAGGGTAAAGGAGACTACACTCCAG	1980
Q	1921	tctcctctgaactctctgtgagtgctgaaagaggtatggaagaaagacacacctccag	1980
D	1981	AGACCCAGGTATGGCAGACTTCAGAGATGGGACAACTTTACAAATTTTCCATAGAG	2040
Q	1981	agacccaggtatgcagagcttcagaaatcggagaaactttacaatcttccaatagagct	2040
D	2041	AAAAATCTTTTGCAGAAGAACCATGACACTTACTTATGATAGCGAATATCTAGATC	2100
Q	2041	aaaaatcttttgcagaagaaagacaatgacacttaactatgacgaatatactagctac	2100
D	2101	ATGAGGGGCAAGTTCTTACCTTCAAAAACAATTCAAAAGAACGTCAGAGAATGGCCAA	2160
Q	2101	atgaggggcaagttcttcaacctcaaaaacaatacgaagaaagtcgaagaatgcccga	2160
D	2161	GCCATGGGGAGAGACTCTCAABAACMTGGAGAACTGGGGGCTCAAAATACCATGAG	2220
Q	2161	gccatgtgggagagagctactcaagaacttggaaactctgtgtgcataaatacactgtgc	2220
D	2221	CGTGTCTTTTGGCCAGAGCTCTACACCTGATGGCTTACGTGTATATTATGGAGAT	2280
Q	2221	cgtgtcttttggccagagctctacacactgtacacactgtgcttaagtcgtatataatggagat	2280
D	2281	GGGCAAAATGTGGCCTTCTCTGAACACAGCCTTGGGGCTCTGTGAACACAGGGGAAT	2340
Q	2281	gggcagaaatgtggcctctctctgaacacagccttggcgtctctctgaaacacaggggaat	2340
D	2341	ATATCTGAGAAATGCTGCTGAACATGAACAAGAATCATGATGATCTCAACTGTGATT	2400
Q	2341	atactggaagaaatgtctgctgaacatgaaacaaagaatcatgtgtactaaacctgtgta	2400
D	2401	AAAAGAAACCATGGCTCAAGCATCTTGAGTCCCATATATGGAAAAAATTATGACGA	2460
Q	2401	aaagaagacaaatgtgcttcagcgactcttgagctcccatcaatgggaaaaaatgtgaca	2460
D	2461	GGCAGGGTAAACATTCAGGATTTCAAAAAACAATTTCTGATGAGAGCTAAATACG	2520
Q	2461	ggcagggtaaacatctcagagacttcaaaaaaacaatctccgtatggaggtataacggtg	2520
D	2521	GACAAATCATTTCTTAACATGTCAAAAGAAAAAGATTTTAATAGCACT 2567	
Q	2521	gcaatcatcttctaactgtcaagaanaaagaatttataagcact 2567	

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